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| (54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM (57) Abstract Novel polynucleotides and the proteins encoded thereby are disclosed. | | |

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SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

5 This application is a continuation-in-part of the following applications:

- (1) provisional application Ser. No. 60/124,916, filed March 17, 1999;
 - (2) provisional application Ser. No. 60/124,808, filed March 17, 1999;
 - (3) provisional application Ser. No. 60/149,639, filed August 17, 1999;
 - (4) provisional application Ser. No. 60/157,247, filed October 1, 1999;
 - 10 (5) provisional application Ser. No. 60/167,824, filed November 29, 1999;
 - (6) provisional application Ser. No. 60/182,711, filed February 15, 2000;
- all of which are incorporated by reference herein.

FIELD OF THE INVENTION

15 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

20 Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case
25 of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid
30 sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number
15 207114;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone vc62_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:2;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260; the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260; the nucleotide sequence of the full-length protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number
- 30 207114;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325; the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325; the nucleotide sequence of the full-length protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having

biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:3, but excluding the poly(A) tail at the
3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone
vp10_1 deposited with the ATCC under accession number 207114;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone
vp10_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp11_1 deposited with the ATCC under
10 accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322; the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322; the nucleotide sequence of the full-length protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the
20 poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322, to a nucleotide sequence
25 corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide
30 200 to nucleotide 322, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number
- 30 207114;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
5 insert of clone vp13_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment
10 comprising eight contiguous amino acids of SEQ ID NO:8;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any
15 one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629; the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629; the nucleotide sequence of the full-length protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp13_1
25 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
30 SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

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(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(bb) the nucleotide sequence of the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp16_1 deposited with the ATCC under
10 accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298; the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298; the nucleotide sequence of the full-length protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number
- 30 207114;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
5 insert of clone vp21_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment
10 comprising eight contiguous amino acids of SEQ ID NO:12;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any
15 one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:11.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607; the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607; the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp21_1
25 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
30 SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from
15 nucleotide 479 to nucleotide 607, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:12;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
vp21_1 deposited with the ATCC under accession number 207114;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477; the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477; the nucleotide sequence of the full-length protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from
30 nucleotide 238 to nucleotide 477, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number
- 30 207114;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
5 insert of clone vq2_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment
10 comprising eight contiguous amino acids of SEQ ID NO:16;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any
15 one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:15.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624; the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624; the nucleotide sequence of the full-length protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq2_1
25 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
30 SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(ab) the nucleotide sequence of the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from
15 nucleotide 106 to nucleotide 624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:16;
(b) a fragment of the amino acid sequence of SEQ ID NO:16; the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
(c) the amino acid sequence encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;
25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090; the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090; the nucleotide sequence of the full-length protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from
30 nucleotide 842 to nucleotide 1090, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:19;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number
- 30 207114;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:19.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275; the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275; the nucleotide sequence of the full-length protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(ab) the nucleotide sequence of the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from
15 nucleotide 159 to nucleotide 275, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:20;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340; the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340; the nucleotide sequence of the full-length protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from
30 nucleotide 230 to nucleotide 340, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:23;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number
- 30 207114;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111; the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111; the nucleotide sequence of the full-length protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114.
- In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from
15 nucleotide 167 to nucleotide 1111, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:24;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc63_1 deposited with the ATCC under
15 accession number 207115;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any
30 one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513; the nucleotide sequence of the full-length protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115; or the nucleotide sequence of a mature protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(bb) the nucleotide sequence of the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:26;

(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number
20 PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
25 insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345; the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345; the nucleotide sequence of the full-length protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb25_1
15 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:28.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and
- (ab) the nucleotide sequence of the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and
- (bb) the nucleotide sequence of the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345, and extending contiguously from a
5 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
10 consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
15 vb25_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably
20 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an
25 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:29 from nucleotide 150 to nucleotide 236;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236; the nucleotide sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236; the nucleotide sequence of the full-length protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362. In other preferred

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embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30
5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:30.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and
 - 20 (ab) the nucleotide sequence of the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and
- (bb) the nucleotide sequence of the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the
- 15 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide
- 20 72 to nucleotide 236. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236, to a nucleotide sequence corresponding to the 3' end of
- 25 said sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- 30 (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence
10 from amino acid 22 to amino acid 31 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb28_1 deposited with the ATCC under
20 accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-
30 362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884; the nucleotide sequence of SEQ ID NO:31
15 from nucleotide 183 to nucleotide 884; the nucleotide sequence of the full-length protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362. In other preferred
20 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a
25 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

20 (bb) the nucleotide sequence of the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID
30 NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206; the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206; the nucleotide sequence of the full-length protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-

362; or the nucleotide sequence of a mature protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-
5 362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a
10 SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced
15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
20 (aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and
(ab) the nucleotide sequence of the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;
25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- 30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
10 of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:35 from nucleotide 98 to nucleotide 253;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the
25 cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA
30 insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253; the nucleotide sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253; the nucleotide sequence of the full-length protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:36.
- Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(ab) the nucleotide sequence of the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424;
- 5 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;
- 10 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;
- 15 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:37.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424; the nucleotide sequence of the full-length

protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide
20 424, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424.

In other embodiments, the present invention provides a composition comprising
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:38;

(b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably
5 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an
10 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vf4_1 deposited with the ATCC under accession
25 number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- 30 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261; the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261; the nucleotide sequence of the full-length protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vf4_1
15 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:40.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
- (ab) the nucleotide sequence of the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- 5 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- 10 (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
- 15 (bb) the nucleotide sequence of the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 20 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

25 NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5' end

30 of said sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261. Also preferably the polynucleotide isolated according to the above

process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
 - 10 (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred
- 15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ
- 20 ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038; the nucleotide sequence of the full-length protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42

having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid
5 sequence from amino acid 239 to amino acid 248 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:41, but excluding the poly(A) tail at the
15 3' end of SEQ ID NO:41; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 vg3_1 deposited with the ATCC under accession number PTA-362;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1575 to
10 nucleotide 3038, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the
15 cDNA sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) a fragment of the amino acid sequence of SEQ ID NO:42, the
25 fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 239 to amino acid 248 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an
5 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363;
- 10 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number
15 PTA-362;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA
20 insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:44;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 30 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363; the nucleotide sequence of the full-length protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363,
25 to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

- (c) the amino acid sequence encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred
- 5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence
- 10 from amino acid 37 to amino acid 46 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo3_1 deposited with the ATCC under
- 20 accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;
- 30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707; the nucleotide sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707; the nucleotide sequence of the full-length protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362. In other preferred
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a
20 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

30 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 5 (aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
- (ab) the nucleotide sequence of the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 10 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 15 (ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
- (bb) the nucleotide sequence of the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;
- 20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the
- 30 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707, and extending contiguously from a nucleotide sequence corresponding to the 5' end

of said sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
5 NO:45 from nucleotide 393 to nucleotide 707, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707.

In other embodiments, the present invention provides a composition comprising
10 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
- (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
- 15 (c) the amino acid sequence encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred
20 acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID NO:46.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:47 from nucleotide 74 to nucleotide 295;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295; the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295; the nucleotide sequence of the full-length protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by

the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
10 ID NO:47.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
20 vo5_1 deposited with the ATCC under accession number PTA-362;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 25 and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:47, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:47; and

- (bb) the nucleotide sequence of the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- 30 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number
20 PTA-362;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
25 insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment
30 comprising eight contiguous amino acids of SEQ ID NO:50;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383; the nucleotide sequence of SEQ ID NO:49
10 from nucleotide 312 to nucleotide 383; the nucleotide sequence of the full-length protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
15 the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a
20 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

25 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the
30 group consisting of:

(aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

- (ab) the nucleotide sequence of the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
- 10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vo6_1 deposited with the ATCC under accession number PTA-362;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide
- 30 45 to nucleotide 383. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383, and extending contiguously from a

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383.

In other embodiments, the present invention provides a composition comprising
5 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the
fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- 10 (c) the amino acid sequence encoded by the cDNA insert of clone
vo6_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred
embodiments, the present invention provides a protein comprising a fragment of the amino
15 acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably
comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ
ID NO:50 having biological activity, the fragment comprising the amino acid sequence
from amino acid 51 to amino acid 60 of SEQ ID NO:50.

20 In one embodiment, the present invention provides a composition comprising an
isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:51 from nucleotide 186 to nucleotide 1739;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:51 from nucleotide 288 to nucleotide 1739;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
length protein coding sequence of clone vo9_1 deposited with the ATCC under
30 accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739; the nucleotide sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739; the nucleotide sequence of the full-length protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by
30 the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52

having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid
5 sequence from amino acid 254 to amino acid 263 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:51, but excluding the poly(A) tail at the
15 3' end of SEQ ID NO:51; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 vo9_1 deposited with the ATCC under accession number PTA-362;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide
10 1739, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:51 from nucleotide 288 to nucleotide 1739, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
- (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred
30 acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 254 to amino acid 263 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:53 from nucleotide 632 to nucleotide 835;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least

5 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835; the nucleotide sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835; the nucleotide sequence of the full-length protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-
10 366; or the nucleotide sequence of a mature protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide
15 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid
20 sequence from amino acid 61 to amino acid 70 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

25 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the
30 3' end of SEQ ID NO:53; and

- (ab) the nucleotide sequence of the cDNA insert of clone
vol1_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the
group consisting of:
- (ba) SEQ ID NO:53, but excluding the poly(A) tail at the
3' end of SEQ ID NO:53; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 vol1_1 deposited with the ATCC under accession number PTA-
366;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID
NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53 , but
25 excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the
polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide
835, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835, to a nucleotide
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide
440 to nucleotide 835. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:53 from nucleotide 632 to nucleotide 835, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
vo11_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence
20 from amino acid 61 to amino acid 70 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:55;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:55 from nucleotide 72 to nucleotide 329;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:55 from nucleotide 120 to nucleotide 329;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
30 length protein coding sequence of clone vo12_1 deposited with the ATCC under
accession number PTA-366;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
25 NO:55 from nucleotide 72 to nucleotide 329; the nucleotide sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329; the nucleotide sequence of the full-length protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366. In other preferred
30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
5 SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(ab) the nucleotide sequence of the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

- (bb) the nucleotide sequence of the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

10 NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329, and extending contiguously from a nucleotide sequence corresponding to the 5' end

15 of said sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329, and extending contiguously from a

20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
- (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
- 30 vo12_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ
5 ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number
20 PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
25 insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (i) a polynucleotide encoding a protein comprising a fragment of the
30 amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:57.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439; the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439; the nucleotide sequence of the full-length protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo13_1
15 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:58.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
- (ab) the nucleotide sequence of the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
- (bb) the nucleotide sequence of the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341; the nucleotide sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341; the nucleotide sequence of the full-length protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366. In other preferred

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embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60
5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:60.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
 - 20 (ab) the nucleotide sequence of the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
- (bb) the nucleotide sequence of the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the
- 15 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide
- 20 96 to nucleotide 341. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341, to a nucleotide sequence corresponding to the 3' end of
- 25 said sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
- 30 (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence
10 from amino acid 36 to amino acid 45 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
20 length protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;
- 25 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-
30 366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599; the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599; the nucleotide sequence of the full-length protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:62;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451; the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451; the nucleotide sequence of the full-length protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-

366; or the nucleotide sequence of a mature protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(bb) the nucleotide sequence of the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:64;

- (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo18_1 deposited with the ATCC under
- 30 accession number PTA-366;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:65.
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- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231; the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231; the nucleotide sequence of the full-length protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
- 20
- 25
- 30 SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:65, but excluding the poly(A) tail at the
10 3' end of SEQ ID NO:65; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;
 - (ii) hybridizing said probe(s) to human genomic DNA in
15 conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
 - 20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:65, but excluding the poly(A) tail at the
25 3' end of SEQ ID NO:65; and
 - (bb) the nucleotide sequence of the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;
 - (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
 - 30 (iii) amplifying human DNA sequences; and
 - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from
15 nucleotide 97 to nucleotide 231, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:66;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- 25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736; the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736; the nucleotide sequence of the full-length protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(bb) the nucleotide sequence of the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
25 corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from

nucleotide 83 to nucleotide 736, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
10 vo19_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
25 NO:69 from nucleotide 158 to nucleotide 1399;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the
30 cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399; the nucleotide sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399; the nucleotide sequence of the full-length protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 211 to amino acid 220 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
5 ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
15 vo22_1 deposited with the ATCC under accession number PTA-366;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
20 probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 vo22_1 deposited with the ATCC under accession number PTA-366;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide
10 1399, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:69 from nucleotide 158 to nucleotide 1399, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred
30 acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 211 to amino acid 220 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo23_1 deposited with the ATCC under
10 accession number PTA-366;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;
- 15 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-
20 366;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment
25 comprising eight contiguous amino acids of SEQ ID NO:72;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 30 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:71.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595; the nucleotide sequence of the full-length protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(ab) the nucleotide sequence of the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

- (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:73 from nucleotide 195 to nucleotide 311;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:73.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311; the nucleotide sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311; the nucleotide sequence of the full-length protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:74.
- Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(bb) the nucleotide sequence of the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- 20 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798; the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798; the nucleotide sequence of the full-length protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

15 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the
20 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide
25 73 to nucleotide 798. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of
30 said sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number
- 30 PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307; the nucleotide sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307; the nucleotide sequence of the full-length protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366. In other preferred
25 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide
30 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
5 ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

15 (ab) the nucleotide sequence of the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

30 (bb) the nucleotide sequence of the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide
10 307, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:77 from nucleotide 101 to nucleotide 307, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred
embodiments, the present invention provides a protein comprising a fragment of the amino
30 acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:79 from nucleotide 94 to nucleotide 228;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228; the nucleotide sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228; the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

- (ab) the nucleotide sequence of the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
- 10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vp23_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but

25 excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228, to a nucleotide

30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:79 from nucleotide 94 to nucleotide 228, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:80;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
vp23_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence
20 from amino acid 26 to amino acid 35 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
30 length protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427; the nucleotide sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427; the nucleotide sequence of the full-length protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82

having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid
5 sequence from amino acid 25 to amino acid 34 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:81, but excluding the poly(A) tail at the
15 3' end of SEQ ID NO:81; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 vq7_1 deposited with the ATCC under accession number PTA-368;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide
10 427, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:81 from nucleotide 308 to nucleotide 427, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
- (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino
30 acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:83 from nucleotide 185 to nucleotide 475;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;
- (i) a polynucleotide encoding a protein comprising a fragment of the
25 amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein
30 of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475; the nucleotide sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475; the nucleotide sequence of the full-length protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and

10 (bb) the nucleotide sequence of the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83, but
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:83. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475, to a nucleotide
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from
30 nucleotide 185 to nucleotide 475, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:84;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:85;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number
- 30 PTA-368;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
5 insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment
10 comprising eight contiguous amino acids of SEQ ID NO:86;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any
15 one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:85.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323; the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323; the nucleotide sequence of the full-length protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq9_1
25 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86
30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

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(aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(ab) the nucleotide sequence of the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

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(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(bb) the nucleotide sequence of the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

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(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323, to a nucleotide
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from
15 nucleotide 141 to nucleotide 323, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:86;
(b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
(c) the amino acid sequence encoded by the cDNA insert of clone
vq9_1 deposited with the ATCC under accession number PTA-368;
25 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
30 of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452; the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368. In other preferred
5 NO:87 from nucleotide 18 to nucleotide 452; the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368. In other preferred
10 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably
15 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.
20 ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
30 vq10_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(bb) the nucleotide sequence of the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
20 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
25 corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452. Also preferably the polynucleotide isolated according to the above
30 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from

nucleotide 72 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
- (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

10 vq10_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably

15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an

20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;
 - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378;
 - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 25 NO:89 from nucleotide 262 to nucleotide 378;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368;

30 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

15 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378; the nucleotide sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378; the nucleotide sequence of the full-length protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368. In other preferred
25 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide
30 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
5 ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
15 vq13_1 deposited with the ATCC under accession number PTA-368;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
20 probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 vq13_1 deposited with the ATCC under accession number PTA-368;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide
10 378, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:89 from nucleotide 262 to nucleotide 378, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino
30 acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 25 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718; the nucleotide sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718; the nucleotide sequence of the full-length protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

- (ab) the nucleotide sequence of the cDNA insert of clone
vq16_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said probe(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the
probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the
group consisting of:
- (ba) SEQ ID NO:91, but excluding the poly(A) tail at the
3' end of SEQ ID NO:91; and
- (bb) the nucleotide sequence of the cDNA insert of clone
15 vq16_1 deposited with the ATCC under accession number PTA-
368;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID
NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91 , but
25 excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the
polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide
718, and extending contiguously from a nucleotide sequence corresponding to the 5' end
of said sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718, to a nucleotide
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide
35 to nucleotide 718. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:91 from nucleotide 173 to nucleotide 718, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
vq16_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence
20 from amino acid 109 to amino acid 118 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:93;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:93 from nucleotide 1 to nucleotide 762;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:93 from nucleotide 70 to nucleotide 762;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
30 length protein coding sequence of clone vq19_1 deposited with the ATCC under
accession number PTA-368;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any
20 one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
25 NO:93 from nucleotide 1 to nucleotide 762; the nucleotide sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762; the nucleotide sequence of the full-length protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368. In other preferred
30 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of
5 SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(ab) the nucleotide sequence of the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

- (bb) the nucleotide sequence of the cDNA insert of clone
vq19_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said primer(s) to human genomic DNA in
conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID
10 NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but
excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the
polynucleotide isolated according to the above process comprises a nucleotide sequence
corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide
762, and extending contiguously from a nucleotide sequence corresponding to the 5' end
15 of said sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762, to a nucleotide
sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide
1 to nucleotide 762. Also preferably the polynucleotide isolated according to the above
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
NO:93 from nucleotide 70 to nucleotide 762, and extending contiguously from a
20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from
nucleotide 70 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of
said sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762.

In other embodiments, the present invention provides a composition comprising
a protein, wherein said protein comprises an amino acid sequence selected from the group
25 consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
- (b) a fragment of the amino acid sequence of SEQ ID NO:94, the
fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
30 vq19_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such
protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ
5 ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number
20 PTA-368;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
25 insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;
- 30 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:95.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792; the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792; the nucleotide sequence of the full-length protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq20_1
15 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:96.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(ab) the nucleotide sequence of the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

10 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(bb) the nucleotide sequence of the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792, and extending contiguously from a
5 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group
10 consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone
15 vq20_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably
20 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an
25 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
30 NO:97 from nucleotide 124 to nucleotide 315;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

20 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:97.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315; the nucleotide sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315; the nucleotide sequence of the full-length protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368. In other preferred

30

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98
5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:98.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
 - 20 (ab) the nucleotide sequence of the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
- (bb) the nucleotide sequence of the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;
- 5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the
- 15 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide
- 20 40 to nucleotide 315. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315, to a nucleotide sequence corresponding to the 3' end of
- 25 said sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
- 30 (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and

(c) the amino acid sequence encoded by the cDNA insert of clone
vq21_1 deposited with the ATCC under accession number PTA-368;
the protein being substantially free from other mammalian proteins. Preferably such
protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred
5 embodiments, the present invention provides a protein comprising a fragment of the amino
acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably
comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ
ID NO:98 having biological activity, the fragment comprising the amino acid sequence
10 from amino acid 41 to amino acid 50 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an
isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:99;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:99 from nucleotide 70 to nucleotide 699;
- (c) a polynucleotide comprising the nucleotide sequence of the full-
length protein coding sequence of clone vr2_1 deposited with the ATCC under
accession number PTA-368;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the
cDNA insert of clone vr2_1 deposited with the ATCC under accession number
PTA-368;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
protein coding sequence of clone vr2_1 deposited with the ATCC under accession
25 number PTA-368;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA
insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;
- (g) a polynucleotide encoding a protein comprising the amino acid
sequence of SEQ ID NO:100;
- 30 (h) a polynucleotide encoding a protein comprising a fragment of the
amino acid sequence of SEQ ID NO:100 having biological activity, the fragment
comprising eight contiguous amino acids of SEQ ID NO:100;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:99.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699; the nucleotide sequence of the full-length protein coding sequence of clone vr2_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vr2_1 deposited with the ATCC under accession number PTA-368. In other preferred
15 embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably
20 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
25 ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and
- (ab) the nucleotide sequence of the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;
- 5 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- 10 (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and
- 15 (bb) the nucleotide sequence of the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 20 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID
- 25 NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699, and extending contiguously from a nucleotide sequence corresponding to the 5' end
- 30 of said sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
 - 5 (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins. Preferably such
- 10 protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ
- 15 ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:101;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number
- 30 PTA-1075;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:101.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394; the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394; the nucleotide sequence of the full-length protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID

NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
5 ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
15 vc69_1 deposited with the ATCC under accession number PTA-1075;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
20 probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 vc69_1 deposited with the ATCC under accession number PTA-1075;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 170 to
10 nucleotide 394, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the
15 cDNA sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
- (b) a fragment of the amino acid sequence of SEQ ID NO:102, the
25 fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an
5 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc71_1 deposited with the ATCC under
20 accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;
- (h) a polynucleotide encoding a protein comprising the amino acid
25 sequence of SEQ ID NO:104;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198; the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198; the nucleotide sequence of the full-length protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

- (ab) the nucleotide sequence of the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
- 10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vc71_1 deposited with the ATCC under accession number PTA-1075;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103 , but
- 25 excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198, to a nucleotide
- 30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:103 from nucleotide 85 to nucleotide 198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- (b) a fragment of the amino acid sequence of SEQ ID NO:104, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
vc71_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence
20 from amino acid 21 to amino acid 30 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:105;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:105 from nucleotide 260 to nucleotide 1552;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
NO:105 from nucleotide 335 to nucleotide 1552;
- (d) a polynucleotide comprising the nucleotide sequence of the full-
30 length protein coding sequence of clone vo27_1 deposited with the ATCC under
accession number PTA-1075;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;
- 5 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;
- 10 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- 15 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any
20 one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID
25 NO:105 from nucleotide 260 to nucleotide 1552; the nucleotide sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552; the nucleotide sequence of the full-length protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075. In other
30 preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

- (ab) the nucleotide sequence of the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID
10 NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552, and extending contiguously from a nucleotide sequence corresponding
15 to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552, and
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552.

In other embodiments, the present invention provides a composition comprising
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably
5 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an
10 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo31_1 deposited with the ATCC under
25 accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;
- 30 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:107.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320; the nucleotide sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320; the nucleotide sequence of the full-length protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:108.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(ab) the nucleotide sequence of the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(bb) the nucleotide sequence of the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255; the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255; the nucleotide sequence of the full-length protein coding sequence of clone vo32_1 deposited with the ATCC under accession

number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession
5 number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid
10 sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:110.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced
15 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(ab) the nucleotide sequence of the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

30 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(bb) the nucleotide sequence of the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:110;

- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:111 from nucleotide 131 to nucleotide 1276;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:111.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276; the nucleotide sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276; the nucleotide sequence of the full-length protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:112.
- Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq23_1 deposited with the ATCC under
15 accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;
- (h) a polynucleotide encoding a protein comprising the amino acid
20 sequence of SEQ ID NO:114;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of
25 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429; the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429; the nucleotide sequence of the full-length protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - 25 (aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and
 - (ab) the nucleotide sequence of the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(bb) the nucleotide sequence of the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

15 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the
20 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113
25 from nucleotide 202 to nucleotide 429. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429, to a nucleotide sequence
30 corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
- 5 (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such
10 protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ
15 ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID
20 NO:115;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113;
- 25 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number
30 PTA-1075;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113; the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113; the nucleotide sequence of the full-length protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID

NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ
5 ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
 - (i) preparing one or more polynucleotide probes that hybridize
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
 - (ab) the nucleotide sequence of the cDNA insert of clone
15 vq24_1 deposited with the ATCC under accession number PTA-1075;
 - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
 - (iii) isolating the DNA polynucleotides detected with the
20 probe(s);
- and
- (b) a process comprising the steps of:
 - (i) preparing one or more polynucleotide primers that hybridize
25 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
 - (ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
 - (bb) the nucleotide sequence of the cDNA insert of clone
30 vq24_1 deposited with the ATCC under accession number PTA-1075;
 - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide
10 1113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID
15 NO:115 from nucleotide 88 to nucleotide 1113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113.

In other embodiments, the present invention provides a composition comprising
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
- (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino
30 acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
10 NO:117 from nucleotide 103 to nucleotide 207;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- (e) a polynucleotide encoding the full-length protein encoded by the
15 cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- 25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
5 25% of the length of SEQ ID NO:117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207; the nucleotide sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207; the nucleotide sequence of the full-length protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-
10 1075; or the nucleotide sequence of a mature protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide
15 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid
20 sequence from amino acid 23 to amino acid 32 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 25 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:117, but excluding the poly(A) tail at
30 the 3' end of SEQ ID NO:117; and

- (ab) the nucleotide sequence of the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize
- 10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 vq26_1 deposited with the ATCC under accession number PTA-1075;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but
- 25 excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207, to a nucleotide
- 30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:117 from nucleotide 103 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;
- (b) a fragment of the amino acid sequence of SEQ ID NO:118, the
10 fragment comprising eight contiguous amino acids of SEQ ID NO:118; and
- (c) the amino acid sequence encoded by the cDNA insert of clone
vq26_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred
15 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence
20 from amino acid 23 to amino acid 32 of SEQ ID NO:118.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions.
25 Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such
30 polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "vc62_1"

A polynucleotide of the present invention has been identified as clone "vc62_1". vc62_1 was isolated from a human fetal brain cDNA library and was identified as
5 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc62_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc62_1 protein").

The nucleotide sequence of vc62_1 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper
10 reading frame and the predicted amino acid sequence of the vc62_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 3 to 15 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted
15 leader/signal sequence not be separated from the remainder of the vc62_1 protein. If the 'G' residue at position 254 of SEQ ID NO:1 were deleted, another potential vc62_1 reading frame and predicted amino acid sequence that would then be encoded by nucleotides 27 to 365 of SEQ ID NO:1 is reported in SEQ ID NO:169.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 vc62_1 should be approximately 4221 bp.

The nucleotide sequence disclosed herein for vc62_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc62_1 demonstrated at least some similarity with sequences identified as AA580489 (nn22a10.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone
25 IMAGE 1084602, mRNA sequence), AF047042 (Homo sapiens citrate synthase mRNA, complete cds), and T04200 (Sugar beet citrate synthase cDNA; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vc62_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc62_1 protein demonstrated at least some similarity to
30 sequences identified as AF047042 (citrate synthase [Homo sapiens]) and R82839 (Sugar beet citrate synthase). Based upon sequence similarity, vc62_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vp10_1"

A polynucleotide of the present invention has been identified as clone "vp10_1". vp10_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp10_1 protein").

The nucleotide sequence of vp10_1 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 19 to 31 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp10_1 protein. If another 'G' residue were inserted in SEQ ID NO:3 after the 'G' residue at position 868, another potential vp10_1 reading frame and predicted amino acid sequence that would be encoded by what would then be nucleotides 6 to 968 of SEQ ID NO:3 is reported in SEQ ID NO:170.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp10_1 should be approximately 1401 bp.

The nucleotide sequence disclosed herein for vp10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp10_1 demonstrated at least some similarity with sequences identified as AA733074 (zg79d07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 399565 3' similar to WP:C15H9.5 CE06834; mRNA sequence). The predicted amino acid sequence disclosed herein for vp10_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp10_1 protein demonstrated at least some similarity to the sequence identified as U56965 (unknown protein [Caenorhabditis elegans]). Based upon sequence similarity, vp10_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vp10_1 protein sequence centered around amino acid 270 of SEQ ID NO:4.

Clone "vp11_1"

A polynucleotide of the present invention has been identified as clone "vp11_1". vp11_1 was isolated from a human adult prostate cDNA library and was identified as
5 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp11_1 protein").

The nucleotide sequence of vp11_1 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper
10 reading frame and the predicted amino acid sequence of the vp11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6. Amino acids 5 to 17 of SEQ ID NO:6 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted
15 leader/signal sequence not be separated from the remainder of the vp11_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp11_1 should be approximately 1329 bp.

The nucleotide sequence disclosed herein for vp11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
20 FASTA search protocols. No hits were found in the database.

Clone "vp13_1"

A polynucleotide of the present invention has been identified as clone "vp13_1". vp13_1 was isolated from a human adult prostate cDNA library and was identified as
25 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp13_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp13_1 protein").

The nucleotide sequence of vp13_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper
30 reading frame and the predicted amino acid sequence of the vp13_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 13 to 25 of SEQ ID NO:8 are a predicted leader/signal sequence, with the predicted mature amino

acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp13_1 protein.

Other potential vp13_1 reading frames and predicted amino acid sequences are
5 encoded by nucleotides 151 to 267 of SEQ ID NO:7, with the encoded amino acid
sequence reported in SEQ ID NO:171, and by nucleotides 209 to 787 of SEQ ID NO:7,
with the encoded amino acid sequence reported in SEQ ID NO:172. Amino acids 1 to 13
of SEQ ID NO:172 are a predicted leader/signal sequence, with the predicted mature
amino acid sequence beginning at amino acid 14. Due to the hydrophobic nature of this
10 predicted leader/signal sequence, it is likely to act as a transmembrane domain should it
not be separated from the remainder of the protein of SEQ ID NO:172. The protein of
SEQ ID NO:172 also demonstrates significant homology to the human Notch protein,
Delta proteins from various species, and other EGF-repeat-containing transmembrane
proteins. A deletion or insertion causing a frame-shift in the nucleotide sequence of SEQ
15 ID NO:7 in the region approximately between nucleotides 208 and 267 of SEQ ID NO:7
could join the reading frames of SEQ ID NO:171 and SEQ ID NO:172 into a single
reading frame encoding an EGF-repeat-containing protein. Further, the region
approximately between nucleotides 605 and 850 may be an alternatively spliced exon.

If the 'A' residue at position 423 of SEQ ID NO:7 were deleted, another potential
20 vp13_1 reading frame and predicted amino acid sequence that would be encoded by what
would then be nucleotides 288 to 503 of SEQ ID NO:7 is reported in SEQ ID NO:173.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
vp13_1 should be approximately 1048 bp.

The nucleotide sequence disclosed herein for vp13_1 was searched against the
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
FASTA search protocols. vp13_1 demonstrated at least some similarity with sequences
identified as AA190865 (zp85b02.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA
clone 626955 3' similar to TR G1336628 G1336628 EGF REPEAT TRANSMEMBRANE
PROTEIN; mRNA sequence), and U57368 (Mus musculus EGF repeat transmembrane
30 protein mRNA, complete cds). The predicted amino acid sequence disclosed herein for
vp13_1 was searched against the GenPept and GeneSeq amino acid sequence databases
using the BLASTX search protocol. The predicted vp13_1 protein demonstrated at least

some similarity to sequences identified as AC004663 (Notch 3 [Homo sapiens]), R28960 (Delta D11), and U57368 (EGF repeat transmembrane protein [Mus musculus]). Based upon sequence similarity, vp13_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential
5 transmembrane domain within the vp13_1 protein sequence centered around amino acid 56 of SEQ ID NO:8.

Clone "vp16_1"

A polynucleotide of the present invention has been identified as clone "vp16_1".
10 vp16_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp16_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp16_1 protein").

The nucleotide sequence of vp16_1 as presently determined is reported in SEQ ID
15 NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp16_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 34 to 46 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted
20 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp16_1 protein. Another potential vp16_1 reading frame and predicted amino acid sequence is encoded by basepairs 1621 to 1839 of SEQ ID NO:9 and is reported in SEQ ID NO:174.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
25 vp16_1 should be approximately 2105 bp.

The nucleotide sequence disclosed herein for vp16_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp16_1 demonstrated at least some similarity with sequences identified as AA523851 (ng31e01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone
30 IMAGE:936408, mRNA sequence). Based upon sequence similarity, vp16_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vp16_1 protein

sequence, one centered around amino acid 36 and another around amino acid 69 of SEQ ID NO:10. The nucleotide sequence of vp16_1 indicates that it may contain an Alu repetitive element.

5 Clone "vp21_1"

A polynucleotide of the present invention has been identified as clone "vp21_1". vp21_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp21_1 is a full-length clone, including the
10 entire coding sequence of a secreted protein (also referred to herein as "vp21_1 protein").

The nucleotide sequence of vp21_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 62 to 74
15 of SEQ ID NO:12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp21_1 protein. Another potential vp21_1 reading frame and predicted amino acid sequence encoded by
20 basepairs 598 to 831 of SEQ ID NO:11 is reported in SEQ ID NO:175. Amino acids 1 to 6 of SEQ ID NO:175 and amino acids 41 to 43 of SEQ ID NO:175 are predicted leader/signal sequences, with the predicted mature amino acid sequences beginning at amino acid 7 or at amino acid 44, respectively.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
25 vp21_1 should be approximately 1538 bp.

The nucleotide sequence disclosed herein for vp21_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp21_1 demonstrated at least some similarity with sequences identified as AC004076 (Homo sapiens chromosome 19, cosmid R30217, complete
30 sequence). The predicted amino acid sequence disclosed herein for vp21_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp21_1 protein demonstrated at least some similarity to

sequences identified as AC003682 (Zinc finger protein F18547_1 [Homo sapiens]) and W19106 (Tat pheromone receptor VN5). Based upon sequence similarity, vp21_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts potential transmembrane domains within the predicted vp21_1 protein sequences, one centered around amino acid 70 of SEQ ID NO:12, and one centered around amino acid 17 of SEQ ID NO:175.

Clone "vp22_1"

A polynucleotide of the present invention has been identified as clone "vp22_1".
10 vp22_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp22_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp22_1 protein").

The nucleotide sequence of vp22_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp22_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 13 to 25 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp22_1 protein. Another potential vp22_1 reading frame and predicted amino acid sequence encoded by basepairs 408 to 1154 of SEQ ID NO:13 is reported in SEQ ID NO:176. Amino acids 40 to 52 of SEQ ID NO:176 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 53. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:176. A frameshift within the nucleotide sequence of SEQ ID NO:13 approximately between nucleotides 163 and 477 could join the openreading frames of SEQ ID NO:14 and SEQ ID NO:176.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp22_1 should be approximately 1718 bp.

The nucleotide sequence disclosed herein for vp22_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp22_1 demonstrated at least some similarity with sequences identified as AA526186 (ni94h03.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone
5 IMAGE:984533, mRNA sequence), AA570505 (nk64h01.s1 NCI_CGAP_Sch1 Homo sapiens cDNA clone IMAGE 1018321, mRNA sequence), AB006085 (Danio rerio mRNA for MINDIN2, complete cds), and T78360 (Human neuronal attachment factor-1 DNA; standard; DNA). The predicted amino acid sequence disclosed herein for vp22_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the
10 BLASTX search protocol. The predicted vp22_1 protein demonstrated at least some similarity to sequences identified as AB006085 (MINDIN2 [Danio rerio]) and W23663 (Human neuronal attachment factor-1). Based upon sequence similarity, vp22_1 proteins and each similar protein or peptide may share at least some activity.

15 Clone "vq2_1"

A polynucleotide of the present invention has been identified as clone "vq2_1". vq2_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq2_1 is a full-length clone, including the entire coding
20 sequence of a secreted protein (also referred to herein as "vq2_1 protein").

The nucleotide sequence of vq2_1 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 4 to 16
25 of SEQ ID NO:16 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq2_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
30 vq2_1 should be approximately 896 bp.

The nucleotide sequence disclosed herein for vq2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. vq2_1 demonstrated at least some similarity with sequences identified as AI203981 (qe76h05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744953 3', mRNA sequence) and T97082 (Human haematopoietic-specific protein (HSP) DNA; standard; DNA). The predicted amino acid sequence disclosed herein
5 for vq2_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq2_1 protein demonstrated at least some similarity to the sequence identified as W35904 (Human haematopoietic-specific protein (HSP)). Based upon sequence similarity, vq2_1 proteins and each similar protein or peptide may share at least some activity.

10

Clone "vq3_1"

A polynucleotide of the present invention has been identified as clone "vq3_1". vq3_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid
15 sequence of the encoded protein. vq3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq3_1 protein").

The nucleotide sequence of vq3_1 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq3_1 protein corresponding
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 11 to 23 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq3_1 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq3_1 should be approximately 1490 bp.

The nucleotide sequence disclosed herein for vq3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The nucleotide
30 sequence of vq3_1 indicates that it may contain an Alu repetitive element.

Clone "vq5_1"

A polynucleotide of the present invention has been identified as clone "vq5_1". vq5_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid
5 sequence of the encoded protein. vq5_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq5_1 protein").

The nucleotide sequence of vq5_1 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq5_1 protein corresponding
10 to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 9 to 21 of SEQ ID NO:20 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq5_1 protein.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq5_1 should be approximately 2207 bp.

The nucleotide sequence disclosed herein for vq5_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq5_1 demonstrated at least some similarity with sequences
20 identified as AQ036276 (CIT-HSP-2331M15.TF CIT-HSP Homo sapiens genomic clone 2331M15, genomic survey sequence) and T24918 (Human gene signature HUMGS07027; standard; cDNA to mRNAP). Based upon sequence similarity, vq5_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts that the signal sequence at residue 22 of SEQ ID NO:20 is also a
25 potential transmembrane domain.

Clone "vq6_1"

A polynucleotide of the present invention has been identified as clone "vq6_1". vq6_1 was isolated from a human adult lung cDNA library and was identified as encoding
30 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq6_1 protein").

The nucleotide sequence of vq6_1 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq6_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 6 to 18 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq6_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq6_1 should be approximately 1875 bp.

The nucleotide sequence disclosed herein for vq6_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq6_1 demonstrated at least some similarity with sequences identified as AA729043 (nw22d09.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241201 similar to contains Alu repetitive element; mRNA sequence). Based upon sequence similarity, vq6_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vq6_1 protein sequence centered around amino acid 37 of SEQ ID NO:22. The nucleotide sequence of vq6_1 indicates that it may contain an Alu repetitive element.

Clone "vr1_1"

A polynucleotide of the present invention has been identified as clone "vr1_1". vr1_1 was isolated from a human adult muscle cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vr1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vr1_1 protein").

The nucleotide sequence of vr1_1 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vr1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 34 to 46 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino

acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vr1_1 protein. The region of SEQ ID NO:23 approximately between nucleotides 1931 and 1977 of SEQ ID NO:23 may be an alternatively spliced exon.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vr1_1 should be approximately 1512 bp.

The nucleotide sequence disclosed herein for vr1_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vr1_1 demonstrated at least some similarity with sequences identified as AL031602 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9; HTGS phase 1), I64695 (Sequence 1 from patent US 5665588), and T35233 (Natural killer lytic associated protein cDNA; standard; cDNA). The predicted amino acid sequence disclosed herein for vr1_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vr1_1 protein demonstrated at least some similarity to sequences identified as R99256 (Natural killer lytic associated protein), and X71642 (GEG-154 gene product [Mus musculus]). Based upon sequence similarity, vr1_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vr1_1 protein sequence centered around amino acid 150 of SEQ ID NO:24.

Clone "vc63_1"

A polynucleotide of the present invention has been identified as clone "vc63_1". vc63_1 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc63_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "vc63_1 protein").

The nucleotide sequence of vc63_1 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc63_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Another potential

vc63_1 reading frame and predicted amino acid sequence encoded by basepairs 528 to 1100 of SEQ ID NO:25 is reported in SEQ ID NO:177. Amino acids 140 to 152 of SEQ ID NO:177 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 153. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:177.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc63_1 should be approximately 2397 bp.

10 The nucleotide sequence disclosed herein for vc63_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc63_1 demonstrated at least some similarity with sequences identified as N66555 (yy69b07.s1 Homo sapiens cDNA clone 278773 3') and T21367 (Human gene signature HUMGS02731; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vc63_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc63_1 protein demonstrated at least some similarity to the sequence identified as Z36948 (D2089.2 [Caenorhabditis elegans]). Based upon sequence similarity, vc63_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the protein sequence of SEQ ID NO:177, centered around amino acid 153 of SEQ ID NO:177.

Clone "vb25_1"

A polynucleotide of the present invention has been identified as clone "vb25_1". vb25_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb25_1 protein").

The nucleotide sequence of vb25_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 5 to 17

of SEQ ID NO:28 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb25_1 protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb25_1 should be approximately 1677 bp.

 The nucleotide sequence disclosed herein for vb25_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb25_1 demonstrated at least some similarity with sequences
10 identified as Z73429 (Human DNA sequence from cosmid cN32F9 on chromosome 22q11.2-qter Contains CpG island). Based upon sequence similarity, vb25_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vb25_1 indicates that it may contain one or more of the following repetitive elements: AC simple repeat, AG simple repeat, ALU, MIR.

15

Clone "vb27_1"

A polynucleotide of the present invention has been identified as clone "vb27_1". vb27_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the
20 amino acid sequence of the encoded protein. vb27_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb27_1 protein").

 The nucleotide sequence of vb27_1 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb27_1 protein corresponding
25 to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 14 to 26 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb27_1 protein.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb27_1 should be approximately 3456 bp.

The nucleotide sequence disclosed herein for vb27_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb27_1 demonstrated at least some similarity with sequences identified as AC005035 (Homo sapiens BAC clone NH0353P23 from 2, complete
5 sequence) and H73579 (yu29f09.r1 Homo sapiens cDNA clone 235241 5'). Based upon sequence similarity, vb27_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vb27_1 indicates that it may contain one or more of the following repetitive elements: ALU, Mer3.

10 Clone "vb28_1"

A polynucleotide of the present invention has been identified as clone "vb28_1". vb28_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb28_1 is a full-length clone, including the
15 entire coding sequence of a secreted protein (also referred to herein as "vb28_1 protein").

The nucleotide sequence of vb28_1 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb28_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 4 to 16
20 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb28_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
25 vb28_1 should be approximately 3008 bp.

The nucleotide sequence disclosed herein for vb28_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb28_1 demonstrated at least some similarity with sequences identified as AA046671 (zf12d09.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA
30 clone IMAGE:376721 5' similar to PIR:A38745 A38745 cell adhesion molecule CD44 precursor - rat; mRNA sequence) and V22687 (DNA encoding a CD44-like protein). The predicted amino acid sequence disclosed herein for vb28_1 was searched against the

GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb28_1 protein demonstrated at least some similarity to sequences identified as W56249 (Amino acid sequence of a CD44-like protein) and X66081 (CD44 [Mus musculus]). Based upon sequence similarity, vb28_1 proteins and each similar protein or
5 peptide may share at least some activity.

Clone "vb29_1"

A polynucleotide of the present invention has been identified as clone "vb29_1". vb29_1 was isolated from a human fetal brain cDNA library and was identified as
10 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb29_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb29_1 protein").

The nucleotide sequence of vb29_1 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper
15 reading frame and the predicted amino acid sequence of the vb29_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 11 to 23 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted
20 leader/signal sequence not be separated from the remainder of the vb29_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb29_1 should be approximately 2970 bp.

The nucleotide sequence disclosed herein for vb29_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
25 FASTA search protocols. vb29_1 demonstrated at least some similarity with sequences identified as AA084068 (zn16d12.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547607 5', mRNA sequence) and AQ418918 (RPCI-11-185K12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185K12, genomic survey sequence). Based upon sequence similarity, vb29_1 proteins and each similar
30 protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vb29_1 protein sequence centered

around amino acid 41 of SEQ ID NO:34. The nucleotide sequence of vb29_1 indicates that it may contain an Alu repetitive element.

Clone "vb30_1"

5 A polynucleotide of the present invention has been identified as clone "vb30_1". vb30_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb30_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb30_1 protein").

10 The nucleotide sequence of vb30_1 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb30_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. Amino acids 15 to 27 of SEQ ID NO:36 are a predicted leader/signal sequence, with the predicted mature amino

15 acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb30_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb30_1 should be approximately 3325 bp.

20 The nucleotide sequence disclosed herein for vb30_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. The nucleotide sequence of vb30_1 indicates that it may contain an Alu repetitive element.

25 Clone "vc67_1"

A polynucleotide of the present invention has been identified as clone "vc67_1". vc67_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc67_1 is a full-length clone, including the

30 entire coding sequence of a secreted protein (also referred to herein as "vc67_1 protein").

The nucleotide sequence of vc67_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vc67_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Another potential vc67_1 reading frame and predicted amino acid sequence encoded by basepairs 3 to 242 of SEQ ID NO:37 is reported in SEQ ID NO:178.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc67_1 should be approximately 2305 bp.

 The nucleotide sequence disclosed herein for vc67_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc67_1 demonstrated at least some similarity with sequences
10 identified as T23222 (Human gene signature HUMGS05018), W87297 (zh67h03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE 417173 3', mRNA sequence), and Z97201 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE). The predicted amino acid sequence disclosed herein for vc67_1 was searched against the GenPept and
15 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc67_1 protein demonstrated at least some similarity to sequences identified as W69427 (Human secreted protein bk291_3) and Z68751 (Similarity to Yeast hypothetical protein YKK0 (SW YKK0_YEAST); cDNA EST EMBL C12578 comes from this gene; cDNA EST yk329g12.5 comes from this gene; cDNA EST yk415). Based upon sequence
20 similarity, vc67_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vc67_1 protein sequence of SEQ ID NO:38, one centered around amino acid 58 and another around amino acid 85 of SEQ ID NO:38.

25 Clone "vf4_1"

 A polynucleotide of the present invention has been identified as clone "vf4_1". vf4_1 was isolated from a human adult heart cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vf4_1 is a full-length clone, including the entire coding
30 sequence of a secreted protein (also referred to herein as "vf4_1 protein").

 The nucleotide sequence of vf4_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vf4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40. Amino acids 5 to 17 of SEQ ID NO:40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vf4_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vf4_1 should be approximately 972 bp.

The nucleotide sequence disclosed herein for vf4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vf4_1 demonstrated at least some similarity with sequences identified as AA813690 (ai71a09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376248 3', mRNA sequence) and V86544 (EST clone AZ285). Based upon sequence similarity, vf4_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vg3_1"

A polynucleotide of the present invention has been identified as clone "vg3_1". vg3_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vg3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vg3_1 protein").

The nucleotide sequence of vg3_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vg3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 13 to 25 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vg3_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vg3_1 should be approximately 3667 bp.

The nucleotide sequence disclosed herein for vg3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vg3_1 demonstrated at least some similarity with sequences identified as AI283122 (qm51h10.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE 1892323 3', mRNA sequence). The predicted amino acid sequence disclosed herein for vg3_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vg3_1 protein demonstrated at least some similarity to sequences identified as U53155 (ZC513.5 [Caenorhabditis elegans]). Based upon sequence similarity, vg3_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts the following transmembrane domains within the vg3_1 protein sequence: four certain transmembrane domains centered around amino acids 78, 133, 156, and 298 of SEQ ID NO:42, respectively; four strongly putative transmembrane domains centered around amino acids 105, 189, 221, and 354 of SEQ ID NO:42, respectively; and six possible transmembrane domains centered around amino acids 262, 272, 322, 367, 432, and 460 of SEQ ID NO:42, respectively. Motifs analysis detected a Crystallins beta and gamma 'Greek key' motif signature around amino acid 52 of SEQ ID NO:42. The nucleotide sequence of vg3_1 indicates that it may contain an Alu repetitive element.

20 Clone "vo2_1"

A polynucleotide of the present invention has been identified as clone "vo2_1". vo2_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo2_1 protein").

The nucleotide sequence of vo2_1 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

30 Another potential vo2_1 reading frame and predicted amino acid sequence encoded by basepairs 95 to 280 of SEQ ID NO:43 is reported in SEQ ID NO:179. Amino acids 9 to 21 of SEQ ID NO:179 are a predicted leader/signal sequence, with the predicted mature

amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:179.

5 Another potential vo2_1 reading frame and predicted amino acid sequence encoded by basepairs 76 to 258 of SEQ ID NO:43 is reported in SEQ ID NO:180. Amino acids 18 to 30 of SEQ ID NO:180 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it
10 not be separated from the remainder of the protein of SEQ ID NO:180.

 Another potential vo2_1 reading frame and predicted amino acid sequence encoded by basepairs 2131 to 2310 of SEQ ID NO:43 is reported in SEQ ID NO:181. Amino acids 38 to 50 of SEQ ID NO:181 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 11; amino acids 19 to 31 of SEQ ID
15 NO:181 are also a possible leader/signal sequence, with the predicted mature amino acid sequence in this case beginning at amino acid 32. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:181.

 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 vo2_1 should be approximately 2903 bp.

 The nucleotide sequence disclosed herein for vo2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo2_1 demonstrated at least some similarity with sequences identified as AI094627 (oy61b07.s1 NCI_CGAP_Brn23 Homo sapiens cDNA clone
25 IMAGE 1670293 3', mRNA sequence). Based upon sequence similarity, vo2_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo3_1"

 A polynucleotide of the present invention has been identified as clone "vo3_1".
30 vo3_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vo3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo3_1 protein").

The nucleotide sequence of vo3_1 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the vo3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 107 to 119 of SEQ ID NO:46 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 120. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the
10 predicted leader/signal sequence not be separated from the remainder of the vo3_1 protein.

If a "C" residue were to be deleted from the nucleotide sequence of SEQ ID NO:45 at either position 917 or position 918, another potential vo3_1 reading frame and predicted amino acid sequence encoded by what would then be basepairs 697 to 1377 of SEQ ID NO:45 is reported in SEQ ID NO:182. Amino acids 62 to 74 of SEQ ID NO:182 are a
15 predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:182.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 vo3_1 should be approximately 1592 bp.

The nucleotide sequence disclosed herein for vo3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo3_1 demonstrated at least some similarity with sequences identified as AA530997 (nj07a06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone
25 IMAGE:985618 3', mRNA sequence), AA683481 (zl55b03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:505805 3', mRNA sequence), D88158 (Pig mRNA for cytochrome b561, complete cds), and V84516 (Human secreted protein gene 106 clone HTOEY16). The predicted amino acid sequence disclosed herein for vo3_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the
30 BLASTX search protocol. The predicted vo3_1 protein demonstrated at least some similarity to sequences identified as U06715 (HCYTO B561 [Homo sapiens]) and W89024 (Polypeptide fragment encoded by gene 156). Based upon sequence similarity, vo3_1

proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the vo3_1 protein sequence, centered around amino acids 35, 75, 113, 146, and 191 of SEQ ID NO:46, respectively.

5

Clone "vo5_1"

A polynucleotide of the present invention has been identified as clone "vo5_1". vo5_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo5_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo5_1 protein").

The nucleotide sequence of vo5_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo5_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 8 to 20 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo5_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo5_1 should be approximately 2487 bp.

The nucleotide sequence disclosed herein for vo5_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo5_1 demonstrated at least some similarity with sequences identified as AA868551 (ak43f09.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1408745 3', mRNA sequence) and AC005500 (complete sequence [Homo sapiens Chromosome 22q11 PAC Clone p52f6 In DGCR Region]). Based upon sequence similarity, vo5_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo5_1 indicates that it may contain an Alu repetitive element.

Clone "vo6_1"

A polynucleotide of the present invention has been identified as clone "vo6_1". vo6_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo6_1 protein").

The nucleotide sequence of vo6_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo6_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino acids 77 to 89 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 90. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo6_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo6_1 should be approximately 1272 bp.

The nucleotide sequence disclosed herein for vo6_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo6_1 demonstrated at least some similarity with sequences identified as AL020989 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 192P9; HTGS phase 1), T34592 (NTII-11 nerve protein coding sequence), and U13617 (Rattus norvegicus Sprague-Dawley plasmolipin mRNA, complete cds). The predicted amino acid sequence disclosed herein for vo6_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo6_1 protein demonstrated at least some similarity to sequences identified as R99799 (NTII-11 nerve protein, facilitates regeneration of nerve cells) and U13617 (plasmolipin [Rattus norvegicus]). Plasmolipin is an 18-kDa proteolipid protein found in kidney and brain, where it is restricted to the apical surface of tubular epithelial cells and to mammalian myelinated tracts, respectively; addition of plasmolipin to lipid bilayers induces the formation of ion channels, which are voltage-dependent and K(+)-selective. (See Fischer and Sapirstein, 1994, *J. Biol. Chem.* 269(40): 24912-24919, which is incorporated by reference herein). Based upon sequence similarity, vo6_1 proteins and

each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the vo6_1 protein sequence, centered around amino acids 14, 42, and 90 of SEQ ID NO:50, respectively.

5 Clone "vo9_1"

A polynucleotide of the present invention has been identified as clone "vo9_1". vo9_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo9_1 is a full-length clone, including the
10 entire coding sequence of a secreted protein (also referred to herein as "vo9_1 protein").

The nucleotide sequence of vo9_1 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 22 to 34
15 of SEQ ID NO: are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo9_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 vo9_1 should be approximately 3331 bp.

The nucleotide sequence disclosed herein for vo9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo9_1 demonstrated at least some similarity with sequences identified as AA936961 (oo65f04.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone
25 IMAGE 1571071 3', mRNA sequence), AF010496 9Rhodobacter capsulatus strain SB1003, partial genome), AL035661 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 568C11, WORKING DRAFT SEQUENCE), and Q24673 (facA gene). The predicted amino acid sequence disclosed herein for vo9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX
30 search protocol. The predicted vo9_1 protein demonstrated at least some similarity to sequences identified as R23968 (facA gene product) and Y15417 (acetate--CoA ligase

[Coprinus cinereus]). Based upon sequence similarity, vo9_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo11_1"

5 A polynucleotide of the present invention has been identified as clone "vo11_1". vo11_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo11_1 protein").

10 The nucleotide sequence of vo11_1 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 52 to 64 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino
15 acid sequence beginning at amino acid 65.

Another potential vo11_1 reading frame and predicted amino acid sequence, encoded by basepairs 18 to 308 of SEQ ID NO:53, is reported in SEQ ID NO:183. Amino acids 10 to 22 of SEQ ID NO:183 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature
20 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:183.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo11_1 should be approximately 1509 bp.

25 The nucleotide sequence disclosed herein for vo11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo11_1 demonstrated at least some similarity with sequences identified as D83866 (similar to none, mRNA sequence). Based upon sequence similarity, vo11_1 proteins and each similar protein or peptide may share at least some activity.

30

Clone "vo12_1"

A polynucleotide of the present invention has been identified as clone "vo12_1". vo12_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo12_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo12_1 protein").

The nucleotide sequence of vo12_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo12_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 4 to 16 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17.

Another potential vo12_1 reading frame and predicted amino acid sequence, encoded by basepairs 107 to 310 of SEQ ID NO:55, is reported in SEQ ID NO:184. Amino acids 14 to 26 and amino acids 18 to 30 of SEQ ID NO:184 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 27 or at amino acid 31, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:184.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo12_1 should be approximately 986 bp.

The nucleotide sequence disclosed herein for vo12_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo12_1 demonstrated at least some similarity with sequences identified as AA444152 (zv51g06.r1 Soares testis NHT Homo sapiens cDNA clone 757210 5', mRNA sequence). Based upon sequence similarity, vo12_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo12_1 protein sequence centered around amino acid 51 of SEQ ID NO:56.

Clone "vo13_1"

A polynucleotide of the present invention has been identified as clone "vo13_1". vo13_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. The vo13_1 clone includes coding sequence of a secreted protein (also referred to herein as "vo13_1 protein").

The nucleotide sequence of vo13_1 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo13_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58. Amino acids 8 to 20 of SEQ ID NO:58 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo13_1 should be approximately 1073 bp.

The nucleotide sequence disclosed herein for vo13_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo13_1 demonstrated at least some similarity with sequences identified as AA988298 (os32a02.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1607018 3', mRNA sequence) and V69614 (Human secreted protein gene 4 clone HE8ND56). The predicted amino acid sequence disclosed herein for vo13_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo13_1 protein demonstrated at least some similarity to sequences identified as W83934 (Human secreted protein from gene 4 clone HE8ND56). Based upon sequence similarity, vo13_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo13_1 protein sequence centered around amino acid 50 of SEQ ID NO:58.

Clone "vo14_1"

A polynucleotide of the present invention has been identified as clone "vo14_1". vo14_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vo14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo14_1 protein").

The nucleotide sequence of vo14_1 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the vo14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60. Amino acids 14 to 26 of SEQ ID NO:60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
10 vo14_1 should be approximately 1605 bp.

The nucleotide sequence disclosed herein for vo14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. Based upon sequence similarity, vo14_1 proteins and each similar protein or peptide may share at least
15 some activity. The nucleotide sequence of vo14_1 indicates that it may contain one or more of the following repetitive elements: Alu, TAAAA repeat.

Clone "vo15_1"

A polynucleotide of the present invention has been identified as clone "vo15_1".
20 vo15_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo15_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo15_1 protein").

The nucleotide sequence of vo15_1 as presently determined is reported in SEQ ID
25 NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo15_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino acids 13 to 25 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26.

30 If a nucleotide were deleted between nucleotide 458 and nucleotide 460 of SEQ ID NO:61, another potential vo15_1 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 90 to 515 of SEQ ID NO:61, is reported in SEQ

ID NO:185. Amino acids 16 to 28 and amino acids 13 to 25 of SEQ ID NO:185 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 29 or at amino acid 26, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:185.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo15_1 should be approximately 2842 bp.

The nucleotide sequence disclosed herein for vo15_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo15_1 demonstrated at least some similarity with sequences identified as AI096756 (qb46e10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE 1703178 3', mRNA sequence). Based upon sequence similarity, vo15_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo15_1 protein sequence centered around amino acid 126 of SEQ ID NO:62. The nucleotide sequence of vo15_1 indicates that it may contain one or more repeat sequences.

Clone "vo16_1"

A polynucleotide of the present invention has been identified as clone "vo16_1". vo16_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo16_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo16_1 protein").

The nucleotide sequence of vo16_1 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo16_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino acids 51 to 63 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 64. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo16_1 protein.

If an "A" or "G" nucleotide were inserted between nucleotides 102 and 103 of SEQ ID NO:63 and an additional "A" residue inserted between nucleotides 271 and 273 of SEQ ID NO:63, another potential vo16_1 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 6 to 338 of SEQ ID NO:63, is reported in SEQ ID NO:186. Amino acids 5 to 17 and amino acids 4 to 16 of SEQ ID NO:186 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 18 or at amino acid 17, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:186.

Another potential vo16_1 reading frame and predicted amino acid sequence, encoded by basepairs 846 to 1061 of SEQ ID NO:63, is reported in SEQ ID NO:187. Amino acids 12 to 24 and amino acids 11 to 23 of SEQ ID NO:187 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 25 or at amino acid 24, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:187.

Nucleotides 1 to 133 of SEQ ID NO:63 are nearly identical to nucleotides 862 to 994 of SEQ ID NO:63, resulting in amino acids 1 to 33 of SEQ ID NO:186 being identical to amino acids 8 to 40 of SEQ ID NO:187.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo16_1 should be approximately 2113 bp.

The nucleotide sequence disclosed herein for vo16_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo16_1 demonstrated at least some similarity with sequences identified as R79825 (y189a06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146386 3', mRNA sequence). Based upon sequence similarity, vo16_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo16_1 protein sequence centered around amino acid 64 of SEQ ID NO:64. The nucleotide sequence of vo16_1 indicates that it may contain an Alu repeat region.

Clone "vo18_1"

A polynucleotide of the present invention has been identified as clone "vo18_1". vo18_1 was isolated from a human adult pancreas cDNA library and was identified as
5 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo18_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo18_1 protein").

The nucleotide sequence of vo18_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper
10 reading frame and the predicted amino acid sequence of the vo18_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 10 to 22 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
15 vo18_1 should be approximately 624 bp.

The nucleotide sequence disclosed herein for vo18_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo18_1 demonstrated at least some similarity with sequences identified as AI198956 (qf66h01.x1 Soares_testis_NHT Homo sapiens cDNA clone
20 IMAGE 1755025 3', mRNA sequence). Based upon sequence similarity, vo18_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo19_1"

A polynucleotide of the present invention has been identified as clone "vo19_1".
25 vo19_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo19_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo19_1 protein").

The nucleotide sequence of vo19_1 as presently determined is reported in SEQ ID
30 NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo19_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 8 to 20

of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo19_1 should be approximately 1957 bp.

5 The nucleotide sequence disclosed herein for vo19_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo19_1 demonstrated at least some similarity with sequences identified as AI524085 (th01e09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2117032 3', mRNA sequence) and V42646 (DNA encoding a human
10 pathogenesis-related protein designated HPRP). The predicted amino acid sequence disclosed herein for vo19_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo19_1 protein demonstrated at least some similarity to sequences identified as U16307 (glioma pathogenesis-related protein [Homo sapiens] and W63115 (A human pathogenesis-related
15 protein designated HPRP). Based upon sequence similarity, vo19_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo22_1"

A polynucleotide of the present invention has been identified as clone "vo22_1".
20 vo22_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo22_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo22_1 protein").

The nucleotide sequence of vo22_1 as presently determined is reported in SEQ ID
25 NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo22_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 6 to 18 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19.

30 If one of the "G" nucleotides at positions 385 and 386 of SEQ ID NO:69 were deleted, and the "G" residue at position 312 of SEQ ID NO:69 changed to a "T", another potential vo22_1 reading frame and predicted amino acid sequence, encoded by what

would then be basepairs 104 to 430 of SEQ ID NO:69, is reported in SEQ ID NO:188. Amino acids 8 to 20, amino acids 7 to 19, amino acids 6 to 18, and amino acids 9 to 21 of SEQ ID NO:188 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 21, or at amino acid 20, or at amino acid 19, or at amino acid 22, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:188.

Another potential vo22_1 reading frame and predicted amino acid sequence, encoded by basepairs 1150 to 1357 of SEQ ID NO:69, is reported in SEQ ID NO:189. Amino acids 3 to 15 of SEQ ID NO:189 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:189.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo22_1 should be approximately 2091 bp.

The nucleotide sequence disclosed herein for vo22_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo22_1 demonstrated at least some similarity with sequences identified as AA706247 (ah28c11.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1240148 3', mRNA sequence) and V34194 (Human secreted protein gene 41 clone HNTME13). The predicted amino acid sequence disclosed herein for vo22_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo22_1 protein demonstrated at least some similarity to sequences identified as AF01644 (No definition line found [Caenorhabditis elegans]) and W75155 (Human secreted protein encoded by gene 41 clone HNTME13). Based upon sequence similarity, vo22_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts 9 potential transmembrane domains within the vo22_1 protein sequence, centered around amino acids 50, 120, 165, 250, 275, 309, 356, 374, and 392 of SEQ ID NO:70, respectively.

Clone "vo23_1"

A polynucleotide of the present invention has been identified as clone "vo23_1". vo23_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo23_1 is a full-length clone, including the
5 entire coding sequence of a secreted protein (also referred to herein as "vo23_1 protein").

The nucleotide sequence of vo23_1 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo23_1 protein corresponding
10 to the foregoing nucleotide sequence is reported in SEQ ID NO:72.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo23_1 should be approximately 2598 bp.

The nucleotide sequence disclosed herein for vo23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
15 FASTA search protocols. vo23_1 demonstrated at least some similarity with sequences identified as T23658 (Human gene signature HUMGS05523), W81246 (zd85b01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347401 5', mRNA sequence), and Z84488 (Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island). Based upon
20 sequence similarity, vo23_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vo23_1 protein sequence, one centered around amino acid 428 and another around amino acid 472 of SEQ ID NO:72.

Clone "vo24_1"

A polynucleotide of the present invention has been identified as clone "vo24_1". vo24_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo24_1 is a full-length clone, including the
30 entire coding sequence of a secreted protein (also referred to herein as "vo24_1 protein").

The nucleotide sequence of vo24_1 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vo24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 10 to 22 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo24_1 should be approximately 3484 bp.

 The nucleotide sequence disclosed herein for vo24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo24_1 demonstrated at least some similarity with sequences
10 identified as AC003117 (***) SEQUENCING IN PROGRESS (***) Human chromosome 1 BAC 308G1 genomic sequence; HTGS phase 1, 3 unordered pieces), V10696 (Human 3.5 kB DNA fragment predicted to contain CH1-9a11-2 gene), and Z94054 (Human DNA sequence from PAC 125H23 on chromosome 1q24-1q25). The predicted amino acid sequence disclosed herein for vo24_1 was searched against the GenPept and GeneSeq
15 amino acid sequence databases using the BLASTX search protocol. The predicted vo24_1 protein demonstrated at least some similarity to sequences identified as W58774 (Human breast cancer gene CH1-9a11-2 protein fragment #1). Based upon sequence similarity, vo24_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo24_1 indicates that it may contain one or more of the following
20 repetitive elements: Alu, Mer33.

Clone "vo25_1"

 A polynucleotide of the present invention has been identified as clone "vo25_1". vo25_1 was isolated from a human adult pancreas cDNA library and was identified as
25 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo25_1 protein").

 The nucleotide sequence of vo25_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper
30 reading frame and the predicted amino acid sequence of the vo25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 11 to 23

of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo25_1 should be approximately 1200 bp.

- 5 The nucleotide sequence disclosed herein for vo25_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo25_1 demonstrated at least some similarity with sequences identified as AI300566 (qn56a09.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE 1902232 3' similar to WP C35D10.1 CE01190 ;, mRNA sequence), V34218
10 (Human secreted protein gene 65 clone HSREG44), and Z55702 (H.sapiens CpG island DNA genomic MseI fragment, clone 58e10, forward read cpg58e10.ft1a). The predicted amino acid sequence disclosed herein for vo25_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo25_1 protein demonstrated at least some similarity to sequences identified as
15 U21324 (similar to *S. cerevisiae* hypothetical protein YKL166 [*Caenorhabditis elegans*]) and W57893 (Protein of clone AT340_1). Based upon sequence similarity, vo25_1 proteins and each similar protein or peptide may share at least some activity. Motifs analysis detected an ATP/GTP-binding site motif A (P-loop) centered around residue 229 of SEQ ID NO:76. The TopPredII computer program predicts a potential transmembrane
20 domain within the vo25_1 protein sequence centered around amino acid 170 of SEQ ID NO:76.

Clone "vo26_1"

- A polynucleotide of the present invention has been identified as clone "vo26_1".
25 vo26_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo26_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo26_1 protein").

- The nucleotide sequence of vo26_1 as presently determined is reported in SEQ ID
30 NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo26_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78. Amino acids 13 to 25

of SEQ ID NO:78 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo26_1 should be approximately 2503 bp.

5 The nucleotide sequence disclosed herein for vo26_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo26_1 demonstrated at least some similarity with sequences identified as AC004707 (Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence), AI160442 (qc08g02.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA
10 clone IMAGE 1709042 3' similar to SWRM02_YEAST P12687 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR; mRNA sequence), and T23473 (Human gene signature HUMGS05312). The predicted amino acid sequence disclosed herein for vo26_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo26_1 protein demonstrated at least
15 some similarity to sequences identified as L37877 (ribosomal protein L27 [Filobasidiella neoformans]). Based upon sequence similarity, vo26_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo26_1 indicates that it may contain a Mir repeat.

20 Clone "vp23_1"

A polynucleotide of the present invention has been identified as clone "vp23_1". vp23_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp23_1 is a full-length clone, including the
25 entire coding sequence of a secreted protein (also referred to herein as "vp23_1 protein").

The nucleotide sequence of vp23_1 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp23_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 5 to 17
30 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted

leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp23_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp23_1 should be approximately 1220 bp.

5 The nucleotide sequence disclosed herein for vp23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp23_1 demonstrated at least some similarity with sequences identified as AL021578 (Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)), predicts a gene like
10 the mouse transcription factor RBP-L). Based upon sequence similarity, vp23_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vp23_1 indicates that it may contain an Alu repetitive element.

Clone "vq7_1"

15 A polynucleotide of the present invention has been identified as clone "vq7_1". vq7_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq7_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq7_1 protein").

20 The nucleotide sequence of vq7_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq7_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 9 to 21 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino
25 acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq7_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq7_1 should be approximately 1326 bp.

30 The nucleotide sequence disclosed herein for vq7_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq7_1 demonstrated at least some similarity with sequences

identified as AA036918 (zk32e03.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 484540 5', mRNA sequence). The predicted amino acid sequence disclosed herein for vq7_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq7_1 protein demonstrated at least some similarity to sequences identified as AF142780 (butyrophilin-like protein [Mus musculus]). Butyrophilin is a glycoprotein of the immunoglobulin superfamily that is secreted in association with the milk-fat-globule membrane from mammary epithelial cells (Ogg *et al.*, 1996, *Mamm. Genome* 7 (12): 900-905, which is incorporated by reference herein). Based upon sequence similarity, vq7_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vq7_1 indicates that it may contain a repetitive element.

Clone "vq8_1"

A polynucleotide of the present invention has been identified as clone "vq8_1". vq8_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq8_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq8_1 protein").

The nucleotide sequence of vq8_1 as presently determined is reported in SEQ ID NO:83, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq8_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84. Amino acids 10 to 22 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq8_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq8_1 should be approximately 695 bp.

The nucleotide sequence disclosed herein for vq8_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq8_1 demonstrated at least some similarity with sequences identified as AA433968 (zw23f07.r1 Soares ovary tumor NbHOT Homo sapiens cDNA

clone 770149 5', mRNA sequence) and V69618 (Human secreted protein gene 8 clone HLHCM89). The predicted amino acid sequence disclosed herein for vq8_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq8_1 protein demonstrated at least some similarity to sequences identified as W83953 (Polypeptide encoded by gene 7 clone HJPDJ64). Based upon sequence similarity, vq8_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq9_1"

10 A polynucleotide of the present invention has been identified as clone "vq9_1". vq9_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq9_1 protein").

15 The nucleotide sequence of vq9_1 as presently determined is reported in SEQ ID NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 5 to 17 of SEQ ID NO:86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq9_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq9_1 should be approximately 1218 bp.

25 The nucleotide sequence disclosed herein for vq9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq9_1 demonstrated at least some similarity with sequences identified as AA769310 (nz39f03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1290173, mRNA sequence). The predicted amino acid sequence disclosed herein for vq9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq9_1 protein demonstrated at least some similarity to sequences identified as U79260 (unknown [Homo sapiens]) and

W48351 (Human breast cancer related protein BCRB2). Based upon sequence similarity, vq9_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq10_1"

5 A polynucleotide of the present invention has been identified as clone "vq10_1". vq10_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq10_1 protein").

10 The nucleotide sequence of vq10_1 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 6 to 18 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino

15 acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq10_1 protein.

 Another potential reading frame, encoded by nucleotides 331 to 834 of SEQ ID NO:87, is reported as the amino acid sequence of SEQ ID NO:190. Amino acids 29 to 41

20 of SEQ ID NO:190 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 42. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:190.

25 If one nucleotide was deleted from the group of nucleotides at positions 330 and 331 of SEQ ID NO:87, another potential reading frame would be created from what would then be nucleotides 18 to 836, with a predicted amino acid sequence reported as SEQ ID NO:191. Amino acids 6 to 18 of SEQ ID NO:191 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the

30 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:191.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq10_1 should be approximately 1516 bp.

The nucleotide sequence disclosed herein for vq10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
5 FASTA search protocols. vq10_1 demonstrated at least some similarity with sequences identified as AA359702 (EST68843 Fetal lung II Homo sapiens cDNA 5' end similar to similar to pulmonary surfactant protein B, mRNA sequence), I08571 (Sequence 14 from Patent WO 8706588), and Q79287 (Human pulmonary surfactant protein B (SPB)). The predicted amino acid sequence disclosed herein for vq10_1 was searched against the
10 GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq10_1 protein demonstrated at least some similarity to sequences identified as J02761 (pulmonary surfactant-associated protein SP-B [Homo sapiens]) and P70664 (6kd pulmonary surfactant protein). Pulmonary surfactant associated proteins such as SP-B promote alveolar stability by lowering the surface tension at the air-liquid interface in
15 the peripheral air spaces. Based upon sequence similarity, vq10_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vq10_1 indicates that it may contain an Alu repetitive element.

Clone "vq13_1"

20 A polynucleotide of the present invention has been identified as clone "vq13_1". vq13_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq13_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq13_1 protein").

25 The nucleotide sequence of vq13_1 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq13_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 10 to 22 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino
30 acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq13_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq13_1 should be approximately 2284 bp.

The nucleotide sequence disclosed herein for vq13_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
5 FASTA search protocols. vq13_1 demonstrated at least some similarity with sequences identified as AA928678 (on48e07.s1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE 1559940 3', mRNA sequence), AB023187 (Homo sapiens mRNA for KIAA0970 protein, complete cds), and T19039 (Human gene signature HUMGS00046). Based upon
10 sequence similarity, vq13_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq16_1"

A polynucleotide of the present invention has been identified as clone "vq16_1". vq16_1 was isolated from a human adult lung cDNA library and was identified as
15 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq16_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq16_1 protein").

The nucleotide sequence of vq16_1 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper
20 reading frame and the predicted amino acid sequence of the vq16_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 34 to 46 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted
25 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq16_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq16_1 should be approximately 1087 bp.

The nucleotide sequence disclosed herein for vq16_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
30 FASTA search protocols. vq16_1 demonstrated at least some similarity with sequences identified as AA400700 (zu70g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743396 5' similar to WP:R05D3.2 CE00281; mRNA sequence). The predicted

amino acid sequence disclosed herein for vq16_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq16_1 protein demonstrated at least some similarity to sequences identified as AF05611 (unknown [Fugu rubripes]). Based upon sequence similarity, vq16_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the vq16_1 protein sequence, centered around amino acids 90, 134, and 174 of SEQ ID NO:92, respectively.

10 Clone "vq19_1"

A polynucleotide of the present invention has been identified as clone "vq19_1". vq19_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq19_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq19_1 protein").

The nucleotide sequence of vq19_1 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq19_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 11 to 23 of SEQ ID NO:94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq19_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq19_1 should be approximately 1833 bp.

The nucleotide sequence disclosed herein for vq19_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq19_1 demonstrated at least some similarity with sequences identified as AA577696 (nn22h03.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1084661 3' similar to contains Alu repetitive element; mRNA sequence. Based upon sequence similarity, vq19_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential

transmembrane domains within the vq19_1 protein sequence centered around amino acid 214 of SEQ ID NO:94. The nucleotide sequence of vq19_1 indicates that it may contain an Alu repetitive element.

5 Clone "vq20_1"

A polynucleotide of the present invention has been identified as clone "vq20_1". vq20_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq20_1 is a full-length clone, including the
10 entire coding sequence of a secreted protein (also referred to herein as "vq20_1 protein").

The nucleotide sequence of vq20_1 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq20_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96. Amino acids 10 to 22
15 of SEQ ID NO:96 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq20_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 vq20_1 should be approximately 1275 bp.

The nucleotide sequence disclosed herein for vq20_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq20_1 demonstrated at least some similarity with sequences identified as AA826249 (of11c04.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone
25 IMAGE 1420806 3' similar to TR Q13445 Q13445 PUTATIVE T1/ST2 RECEPTOR BINDING PROTEIN PRECURSOR; mRNA sequence), AI129838 (qc49h11.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:1712997 3' similar to TR:Q13445 Q13445 PUTATIVE T1/ST2 RECEPTOR BINDING PROTEIN PRECURSOR; mRNA sequence), U41805 (Mus musculus putative T1/ST2 receptor
30 binding protein precursor mRNA, partial cds), and V17729 (Human T1 receptor-like ligand II cDNA). The predicted amino acid sequence disclosed herein for vq20_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted vq20_1 protein demonstrated at least some similarity to sequences identified as U41804 (putative T1/ST2 receptor binding protein precursor [Homo sapiens]) and W48335 (Human T1 receptor-like ligand II). T1/ST2 is a receptor-like molecule homologous to the type I interleukin-1 receptor (Gayle *et al.*, 1996, *J. Biol. Chem.* **271** (10): 5784-5789, which is incorporated by reference herein). Based upon sequence similarity, vq20_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vq20_1 protein sequence centered around amino acid 208 of SEQ ID NO:96.

10

Clone "vq21_1"

A polynucleotide of the present invention has been identified as clone "vq21_1". vq21_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq21_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq21_1 protein").

The nucleotide sequence of vq21_1 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Amino acids 16 to 28 of SEQ ID NO:98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq21_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq21_1 should be approximately 1230 bp.

The nucleotide sequence disclosed herein for vq21_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq21_1 demonstrated at least some similarity with sequences identified as AA149768 (zo01g05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE 566456 3' similar to contains Alu repetitive element; mRNA sequence), AC005282 (Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4

unordered pieces), T25413 (Human gene signature HUMGS07579). The predicted amino acid sequence disclosed herein for vq21_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq21_1 protein demonstrated at least some similarity to sequences identified as U67577 (cell
5 division protein FtsJ [Methanococcus jannaschii]). Based upon sequence similarity, vq21_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vr2_1"

A polynucleotide of the present invention has been identified as clone "vr2_1".
10 vr2_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vr2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vr2_1 protein").

The nucleotide sequence of vr2_1 as presently determined is reported in SEQ ID
15 NO:99. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vr2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vr2_1 should be approximately 1382 bp.

20 The nucleotide sequence disclosed herein for vr2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant similarities were identified in the databases. The TopPredII computer program predicts a potential transmembrane domain within the vr2_1 protein sequence centered around amino acid 85 of SEQ ID NO:100. The nucleotide
25 sequence of vr2_1 indicates that it may contain one or more of the following repetitive elements: Alu, MER2, MER4B.

Clone "vc69_1"

A polynucleotide of the present invention has been identified as clone "vc69_1".
30 vc69_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vc69_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc69_1 protein").

The nucleotide sequence of vc69_1 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper
5 reading frame and the predicted amino acid sequence of the vc69_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. Amino acids 7 to 19 of SEQ ID NO:102 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the
10 predicted leader/signal sequence not be separated from the remainder of the vc69_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc69_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for vc69_1 was searched against the
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc69_1 demonstrated at least some similarity with sequences identified as AB023138 (Homo sapiens mRNA for KIAA0921 protein, partial cds), and AI421941 (tf45c01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE 2099136 3' similar to TR Q63376 Q63376 NEUREXIN II-BETA-A PRECURSOR; mRNA
20 sequence). The predicted amino acid sequence disclosed herein for vc69_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc69_1 protein demonstrated at least some similarity to sequences identified as AB02313 (KIAA0921 protein [Homo sapiens]), and various isoforms of *Rattus norvegicus* neurexin II protein. Based upon sequence similarity,
25 vc69_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vc71_1"

A polynucleotide of the present invention has been identified as clone "vc71_1". vc71_1 was isolated from a human fetal brain cDNA library and was identified as
30 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc71_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc71_1 protein").

The nucleotide sequence of vc71_1 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc71_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104. Amino acids 2 to 14 of SEQ ID NO:104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc71_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc71_1 should be approximately 760 bp.

 The nucleotide sequence disclosed herein for vc71_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc71_1 demonstrated at least some similarity with sequences identified as AI393859 (tg65f04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 2113663 3', mRNA sequence) and AL050018 (Homo sapiens mRNA; cDNA DKFZp564B116 (from clone DKFZp564B116)). Based upon sequence similarity, vc71_1 proteins and each similar protein or peptide may share at least some activity.

20 Clone "vo27_1"

 A polynucleotide of the present invention has been identified as clone "vo27_1". vo27_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo27_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo27_1 protein").

 The nucleotide sequence of vo27_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo27_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106. Amino acids 13 to 25 of SEQ ID NO:106 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the

predicted leader/signal sequence not be separated from the remainder of the vo27_1 protein.

Another potential reading frame, encoded by nucleotides 1665 to 1844 of SEQ ID NO:105, is reported as the amino acid sequence of SEQ ID NO:192. Amino acids 4 to 16 of SEQ ID NO:192 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17; amino acids 28 to 40 of SEQ ID NO:192 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 41. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:192.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo27_1 should be approximately 2433 bp.

The nucleotide sequence disclosed herein for vo27_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo27_1 demonstrated at least some similarity with sequences identified as AC007621 (Homo sapiens clone RPC11-757G14, WORKING DRAFT SEQUENCE, 142 unordered pieces), AI207832 (ao89g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE 1953092 3' similar to contains Alu repetitive element; mRNA sequence), and X80059 (Human PRO361 nucleotide sequence). Based upon sequence similarity, vo27_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo27_1 protein sequence centered around amino acid 400 of SEQ ID NO:106. The nucleotide sequence of vo27_1 indicates that it may contain an Alu repetitive element.

Clone "vo31_1"

A polynucleotide of the present invention has been identified as clone "vo31_1". vo31_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo31_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo31_1 protein").

The nucleotide sequence of vo31_1 as presently determined is reported in SEQ ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo31_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108. Amino acids 7 to 19 of SEQ ID NO:108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo31_1 protein.

10 Another potential reading frame, encoded by nucleotides 1937 to 3007 of SEQ ID NO:107, is reported as the amino acid sequence of SEQ ID NO:193.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo31_1 should be approximately 3222 bp.

The nucleotide sequence disclosed herein for vo31_1 was searched against the
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo31_1 demonstrated at least some similarity with sequences identified as AF022147 (Rattus norvegicus uterus-ovary specific putative transmembrane protein (uo) mRNA, complete cds), AI417638 (tg80e01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 2115096 3' similar to TR O35360 O35360 UTERUS-
20 OVARY SPECIFIC PUTATIVE TRANSMEMBRANE PROTEIN; mRNA sequence), and X52248 (Protein PRO257 cDNA clone DNA35841-1173). The predicted amino acid sequence disclosed herein for vo31_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo31_1 protein demonstrated at least some similarity to sequences identified as AF02214
25 (uterus-ovary specific putative transmembrane protein [Rattus norvegicus]) and Y13377 (Amino acid sequence of protein PRO257). Based upon sequence similarity, vo31_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the protein sequence of SEQ ID NO:193, centered around amino acid 328 of SEQ ID NO:193.
30 Hidden markov model analysis indicates the presence of Zona-pellucida-like domains at amino acids 26-115 and 146-273 of SEQ ID NO:193. The nucleotide sequence of vo31_1 indicates that it may contain a Mer5a repetitive element.

Clone "vo32_1"

A polynucleotide of the present invention has been identified as clone "vo32_1". vo32_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo32_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo32_1 protein").

The nucleotide sequence of vo32_1 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo32_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110. Amino acids 4 to 16 of SEQ ID NO:110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo32_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo32_1 should be approximately 1868 bp.

The nucleotide sequence disclosed herein for vo32_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo32_1 demonstrated at least some similarity with sequences identified as AF028740 (Mus musculus olfactomedin mRNA, complete cds), AI078144 (oz30b06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE 1676819 3' similar to TR Q99784 Q99784 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN; mRNA sequence), AI869993 (wl63e09.x1 NCI_CGAP Brn25 Homo sapiens cDNA clone IMAGE:2429608 3' similar to SW:NOMR_HUMAN Q99784 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN; mRNA sequence), and V34217 (Human secreted protein gene 64 clone HSLDJ95). The predicted amino acid sequence disclosed herein for vo32_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo32_1 protein demonstrated at least some similarity to sequences identified as U03416 (neuronal olfactomedin-related ER localized protein [Rattus norvegicus]) and W75120 (Human secreted protein encoded by gene 64 clone HSLDJ95). Based upon

sequence similarity, vo32_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo33_1"

5 A polynucleotide of the present invention has been identified as clone "vo33_1". vo33_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo33_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo33_1 protein").

10 The nucleotide sequence of vo33_1 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo33_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 5 to 17 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature
15 amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo33_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone
20 vo33_1 should be approximately 2879 bp.

The nucleotide sequence disclosed herein for vo33_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo33_1 demonstrated at least some similarity with sequences identified as AI225613 (uj13e01.y1 Sugano mouse kidney mkia Mus musculus cDNA
25 clone IMAGE:1907928 5' similar to TR:Q14624 Q14624 INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN; mRNA sequence) and X80054 (Human PRO354 nucleotide sequence). The predicted amino acid sequence disclosed herein for vo33_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo33_1 protein
30 demonstrated at least some similarity to sequences identified as D38535 (PK-120 precursor [Homo sapiens]), Y11545 (inter-alpha-inhibitor heavy-chain H2 [Sus scrofa]), and the H2 proteins of several species, including *Homo sapiens*. Based upon sequence similarity,

vo33_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo33_1 protein sequence centered around amino acid 386 of SEQ ID NO:112. The nucleotide sequence of vo33_1 indicates that it may contain an Alu repetitive element.

5

Clone "vq23_1"

A polynucleotide of the present invention has been identified as clone "vq23_1". vq23_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq23_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq23_1 protein").

The nucleotide sequence of vq23_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq23_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 18 to 30 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq23_1 protein.

Another potential reading frame, encoded by nucleotides 1012 to 1518 of SEQ ID NO:113, is reported as the amino acid sequence of SEQ ID NO:194. Amino acids 83 to 94 of SEQ ID NO:194 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 95. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of protein of SEQ ID NO:194.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq23_1 should be approximately 1793 bp.

The nucleotide sequence disclosed herein for vq23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq23_1 demonstrated at least some similarity with sequences

identified as AA625521 (af72f02.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 1047579 5', mRNA sequence) and AC002364 (Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence). Based upon sequence similarity, vq23_1 proteins and each similar
5 protein or peptide may share at least some activity. The nucleotide sequence of vq23_1 indicates that it may contain an Alu repetitive element.

Clone "vq24_1"

A polynucleotide of the present invention has been identified as clone "vq24_1".
10 vq24_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq24_1 protein").

The nucleotide sequence of vq24_1 as presently determined is reported in SEQ ID
15 NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116. Amino acids 5 to 17 of SEQ ID NO:116 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the
20 predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq24_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq24_1 should be approximately 2168 bp.

25 The nucleotide sequence disclosed herein for vq24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq24_1 demonstrated at least some similarity with sequences identified as N29315 (yx43d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264491 5' similar to SP:SW:FCG1_HUMAN P12315 HIGH AFFINITY
30 IMMUNOGLOBULIN GAMMA FC RECEPTOR I 'B FORM' PRECURSOR; mRNA sequence). The predicted amino acid sequence disclosed herein for vq24_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX

search protocol. The predicted vq24_1 protein demonstrated at least some similarity to sequences identified as AF14317 (high affinity immunoglobulin gamma Fc receptor I [Mus musculus]) and R12428 (Hybrid Fc(gamma)RII/I receptor). Based upon sequence similarity, vq24_1 proteins and each similar protein or peptide may share at least some activity. Hidden markov model analysis detects immunoglobulin superfamily signatures in the vq24_1 protein sequence from amino acid 92 to amino acid 145, and from amino acid 185 to amino acid 242, of SEQ ID NO:116. The nucleotide sequence of vq24_1 indicates that it may contain one or more of the following repetitive elements: Mer, MLT1a.

10

Clone "vq26_1"

A polynucleotide of the present invention has been identified as clone "vq26_1". vq26_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq26_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq26_1 protein").

The nucleotide sequence of vq26_1 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq26_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118. Amino acids 9 to 21 of SEQ ID NO:118 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq26_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq26_1 should be approximately 1419 bp.

The nucleotide sequence disclosed herein for vq26_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq26_1 demonstrated at least some similarity with sequences identified as AA191552 (zp82g04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE 626742 3', mRNA sequence) and AA573741 (nk07a05.s1 NCI_CGAP_Co2

Homo sapiens cDNA clone IMAGE:1012784 3', mRNA sequence). Based upon sequence similarity, vq26_1 proteins and each similar protein or peptide may share at least some activity.

5 Deposit of Clones

Clones vc62_1, vp10_1, vp11_1, vp13_1, vp16_1, vp21_1, vp22_1, vq2_1, vq3_1, vq5_1, vq6_1, and vr1_1 were deposited on February 17, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession
10 number ATCC 207114, from which each clone comprising a particular polynucleotide is obtainable.

Clone vc63_1 was deposited on February 17, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number
15 ATCC 207115, from which the vc63_1 clone comprising a particular polynucleotide is obtainable.

Clones vb25_1, vb27_1, vb28_1, vb29_1, vb30_1, vc67_1, vf4_1, vg3_1, vo2_1, vo3_1, vo5_1, vo6_1, and vo9_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia
20 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-362, from which each clone comprising a particular polynucleotide is obtainable.

Clones vo11_1, vo12_1, vo13_1, vo14_1, vo15_1, vo16_1, vo18_1, vo19_1, vo22_1, vo23_1, vo24_1, vo25_1, and vo26_1 were deposited on July 15, 1999 with the
25 ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-366, from which each clone comprising a particular polynucleotide is obtainable.

Clones vp23_1, vq7_1, vq8_1, vq9_1, vq10_1, vq13_1, vq16_1, vq19_1, vq20_1, vq21_1, and vr2_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.)
30

as an original deposit under the Budapest Treaty and were given the accession number PTA-368, from which each clone comprising a particular polynucleotide is obtainable.

Clones vc69_1, vc71_1, vo27_1, vo31_1, vo32_1, vo33_1, vq23_1, vq24_1, and vq26_1 were deposited on December 21, 1999 with the ATCC (American Type Culture
5 Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-1075, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified
10 in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in these composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or
15 pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* **19**: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* **9**: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13
20 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed
25 from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences
30 provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

| | <u>Clone</u> | <u>Probe Sequence</u> |
|----|--------------|-----------------------|
| | vc62_1 | SEQ ID NO:119 |
| | vp10_1 | SEQ ID NO:120 |
| | vp11_1 | SEQ ID NO:121 |
| 5 | vp13_1 | SEQ ID NO:122 |
| | vp16_1 | SEQ ID NO:123 |
| | vp21_1 | SEQ ID NO:124 |
| | vp22_1 | SEQ ID NO:125 |
| | vq2_1 | SEQ ID NO:126 |
| 10 | vq3_1 | SEQ ID NO:127 |
| | vq5_1 | SEQ ID NO:128 |
| | vq6_1 | SEQ ID NO:129 |
| | vr1_1 | SEQ ID NO:130 |
| | vc63_1 | SEQ ID NO:131 |
| 15 | vb25_1 | SEQ ID NO:132 |
| | vb27_1 | SEQ ID NO:133 |
| | vb28_1 | SEQ ID NO:134 |
| | vb29_1 | SEQ ID NO:135 |
| | vb30_1 | SEQ ID NO:136 |
| 20 | vc67_1 | SEQ ID NO:137 |
| | vf4_1 | SEQ ID NO:138 |
| | vg3_1 | SEQ ID NO:139 |
| | vo2_1 | SEQ ID NO:140 |
| | vo3_1 | SEQ ID NO:141 |
| 25 | vo5_1 | SEQ ID NO:142 |
| | vo6_1 | SEQ ID NO:143 |
| | vo9_1 | SEQ ID NO:144 |
| | vo11_1 | SEQ ID NO:145 |
| | vo12_1 | SEQ ID NO:146 |
| 30 | vo13_1 | SEQ ID NO:147 |
| | vo14_1 | SEQ ID NO:148 |
| | vo15_1 | SEQ ID NO:149 |

| | | |
|----|--------|---------------|
| | vo16_1 | SEQ ID NO:150 |
| | vo18_1 | SEQ ID NO:151 |
| | vo19_1 | SEQ ID NO:152 |
| | vo22_1 | SEQ ID NO:153 |
| 5 | vo23_1 | SEQ ID NO:154 |
| | vo24_1 | SEQ ID NO:155 |
| | vo25_1 | SEQ ID NO:156 |
| | vo26_1 | SEQ ID NO:157 |
| | vp23_1 | SEQ ID NO:158 |
| 10 | vq7_1 | SEQ ID NO:159 |
| | vq8_1 | SEQ ID NO:160 |
| | vq9_1 | SEQ ID NO:161 |
| | vq10_1 | SEQ ID NO:162 |
| | vq13_1 | SEQ ID NO:163 |
| 15 | vq16_1 | SEQ ID NO:164 |
| | vq19_1 | SEQ ID NO:165 |
| | vq20_1 | SEQ ID NO:166 |
| | vq21_1 | SEQ ID NO:167 |
| | vr2_1 | SEQ ID NO:168 |
| 20 | | |

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ -³²P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for

labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting
5 probe should be approximately 4×10^6 dpm/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 μ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh
10 L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 μ g/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

15 Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 μ g/ml of yeast RNA, and 10 mM EDTA
20 (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1×10^6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle
25 shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated
30 using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* **15**(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* **62**(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* **58**: 1-39; all of which are incorporated by reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA interference" or "RNAi"; Fire *et al.*, 1998, *Nature* **391** (6669): 806-811; Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* **95** (26): 15502-15507; and Sharp, 1999, *Genes Dev.* **13** (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European

Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through
5 insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* **14**(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* **90**(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* **91**(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably
10 detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* **336**: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the
15 study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part
20 or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of
25 transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most
30 preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid

sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any

combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

5 Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence
10 identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize
15 overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla*
20 *gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the
25 identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuáñez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and
30 Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least
5 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided
10 herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced
15 stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

| | Stringency Condition | Polynucleotide Hybrid | Hybrid Length (bp) [‡] | Hybridization Temperature and Buffer [†] | Wash Temperature and Buffer [†] |
|----|----------------------|-----------------------|---------------------------------|---|--|
| 5 | A | DNA:DNA | ≥ 50 | 65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide | 65°C; 0.3xSSC |
| | B | DNA:DNA | <50 | T _B *; 1xSSC | T _B *; 1xSSC |
| | C | DNA:RNA | ≥ 50 | 67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide | 67°C; 0.3xSSC |
| | D | DNA:RNA | <50 | T _D *; 1xSSC | T _D *; 1xSSC |
| | E | RNA:RNA | ≥ 50 | 70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide | 70°C; 0.3xSSC |
| | F | RNA:RNA | <50 | T _F *; 1xSSC | T _F *; 1xSSC |
| 10 | G | DNA:DNA | ≥ 50 | 65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide | 65°C; 1xSSC |
| | H | DNA:DNA | <50 | T _H *; 4xSSC | T _H *; 4xSSC |
| | I | DNA:RNA | ≥ 50 | 67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide | 67°C; 1xSSC |
| | J | DNA:RNA | <50 | T _J *; 4xSSC | T _J *; 4xSSC |
| | K | RNA:RNA | ≥ 50 | 70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide | 67°C; 1xSSC |
| | L | RNA:RNA | <50 | T _L *; 2xSSC | T _L *; 2xSSC |
| 15 | M | DNA:DNA | ≥ 50 | 50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide | 50°C; 2xSSC |
| | N | DNA:DNA | <50 | T _N *; 6xSSC | T _N *; 6xSSC |
| | O | DNA:RNA | ≥ 50 | 55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide | 55°C; 2xSSC |
| | P | DNA:RNA | <50 | T _P *; 6xSSC | T _P *; 6xSSC |
| | Q | RNA:RNA | ≥ 50 | 60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide | 60°C; 2xSSC |
| | R | RNA:RNA | <50 | T _R *; 4xSSC | T _R *; 4xSSC |

[‡]: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[†]: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable

bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope.

One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

10 The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell*

75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* **94**: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to
5 determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue
10 differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or
15 small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning:
20 A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

25 Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid
30 preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors
5 discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G,
10 M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek,
15 D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992;
20 Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and
25 Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine
30 Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al.,

Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of
5 human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

10 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience
15 (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

20

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies
25 and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral,
30 bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,

in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems.

10 Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction

15 of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is

20 distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without

25 limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated

30 through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble,

monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the

disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine
5 autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy.
10 Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B
15 lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro*
20 activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory
25 signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present
30 invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an

expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to
5 target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II
10 molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface.
15 Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the
20 activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured
25 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte
30 Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol.

- 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

- Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in:
- 10 Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation,
- 15 those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J.
- 20 Immunol. 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology*
- 25 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

- 30 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz

et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

- 5 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

10 Hematopoiesis Regulating Activity

- A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and
- 15 proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for
- 20 example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic
- 25 stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction
- 30 with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

5 Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

10 Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic
15 colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term
20 bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

25

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions
30 and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone

fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue.

5 More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include
10 mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of
15 non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac)
20 and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or
25 regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

5 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

10 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present
15 invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β
20 group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

25 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al.,
30 Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

10 A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known
15 assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and
20 beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

30 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation

and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels
5 (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis
10 Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors,
15 receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs
20 involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

25 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and
30 Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin
15 lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus
25 vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The
30 cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin

so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the

circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

- Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

- In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities.
- 10 A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit
- 15 tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

- A protein of the invention may also exhibit one or more of the following additional
- 20 activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution,
- 25 change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress,
- 30 cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic

lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen
5 in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including
10 without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the
15 effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF,
20 thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may
25 be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers
30 or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination
5 with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the
10 attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a
15 variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule,
20 powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal
25 or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein
30 of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the

term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where
5 abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage,
10 tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or
15 tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition
20 would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability,
25 mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined,
30 such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics.

Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

5 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

10 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of
15 acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are
20 prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

 In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor
25 (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

 The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

30 The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be

formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:1;
- (b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260;
- (c) the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:1.

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
 - (a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and
 - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. An isolated polynucleotide encoding the protein of claim 6.
8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114.
9. A protein comprising an amino acid sequence selected from the group consisting of:
 - (a) the amino acid sequence of SEQ ID NO:2;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;the protein being substantially free from other mammalian proteins.
10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:3;
- (b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325;
- (c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:5;
- (b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322;
- (c) the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:5.

15. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:7;

(b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629;

(c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:7.

17. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;
the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:9;

(b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298;

(c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:11;
- (b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607;
- (c) the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:13;
- (b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477;
- (c) the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:13.

23. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:15;
- (b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624;
- (c) the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:17;

(b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090;

(c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:19;
- (b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275;
- (c) the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;

- (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114; the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:21;
- (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340;
- (c) the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;
- the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:23;
- (b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111;
- (c) the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:25;

(b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:26;

(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:27;

(b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345;

(c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:29;
- (b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236;
- (c) the nucleotide sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;

- (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:31;
- (b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884;
- (c) the nucleotide sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:33;
- (b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206;
- (c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.

45. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:36;

(b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:37;
- (b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
- (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362; the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:39;
- (b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261;
- (c) the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:41;
- (b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038;
- (c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:43;

(b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:45;

(b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707;

(c) the nucleotide sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;

- (f) the nucleotide sequence of a mature protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;
- the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:47;
- (b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295;

- (c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:49;
- (b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383;
- (c) the nucleotide sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- (c) the amino acid sequence encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:51;
- (b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739;
- (c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:51.

61. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:52;

(b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:53;

(b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835;

(c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vol1_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone vol1_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:55;

(b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329;

(c) the nucleotide sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:57;
- (b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439;
- (c) the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:59;
- (b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341;
- (c) the nucleotide sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:61;
- (b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599;
- (c) the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:63;

(b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451;

(c) the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:63.

73. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:64;

(b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231;
- (c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.

75. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;

- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:67;
- (b) the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736;
- (c) the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:67.

77. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:69;
- (b) the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399;
- (c) the nucleotide sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:70;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:69.

79. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:70;

(b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:71;

(b) the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:71.

81. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

(b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:73;

(b) the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311;

(c) the nucleotide sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:73.

83. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:74;

(b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:75;
- (b) the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798;
- (c) the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:75.

85. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;

- (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:27;
- (b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 26 to nucleotide 307;
- (c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 307;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

87. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;
- the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:79;
- (b) the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228;
- (c) the nucleotide sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:79.

89. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:80;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

90. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:81;
- (b) the nucleotide sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427;
- (c) the nucleotide sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:81.

91. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:82;

(b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

92. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:83;
- (b) the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475;
- (c) the nucleotide sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:84;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:83.

93. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:84;

(b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

94. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:85;

(b) the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323;

(c) the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:86;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:85.

95. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:86;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

96. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:87;
- (b) the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452;
- (c) the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:88;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:87.

97. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:88;

(b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

98. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:89;

(b) the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378;

(c) the nucleotide sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:89.

99. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:90;

(b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

100. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:91;
- (b) the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718;
- (c) the nucleotide sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:91.

101. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;

(b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

102. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:93;

(b) the nucleotide sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762;

(c) the nucleotide sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:93.

103. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

104. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:95;
- (b) the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792;
- (c) the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:95.

105. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:96;

(b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

106. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:97;

(b) the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315;

(c) the nucleotide sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:98;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:97.

107. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:98;

(b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

108. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:99;
- (b) the nucleotide sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone vr2_1 deposited with the ATCC under accession number PTA-368;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:99.

109. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;
- the protein being substantially free from other mammalian proteins.

110. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:101;
- (b) the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394;
- (c) the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone PTA-1075 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:101.

111. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;

(b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

112. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:103;

(b) the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198;

(c) the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:103.

113. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

114. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:105;
- (b) the nucleotide sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552;
- (c) the nucleotide sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:105.

115. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

116. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:107;
- (b) the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320;
- (c) the nucleotide sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:107.

117. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

118. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:109;
- (b) the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255;
- (c) the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:109.

119. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:110;

(b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

120. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:111;

(b) the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276;

(c) the nucleotide sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:111.

121. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
 - (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
 - (c) the amino acid sequence encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;
- the protein being substantially free from other mammalian proteins.

122. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:113;
- (b) the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429;
- (c) the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:114;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:113.

123. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:114;

(b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

124. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:115;

(b) the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113;

(c) the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:116;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:115.

125. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:116;

(b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

126. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:117;
- (b) the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207;
- (c) the nucleotide sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- (f) the nucleotide sequence of a mature protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:117.

127. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075; the protein being substantially free from other mammalian proteins.

Fig. 1A

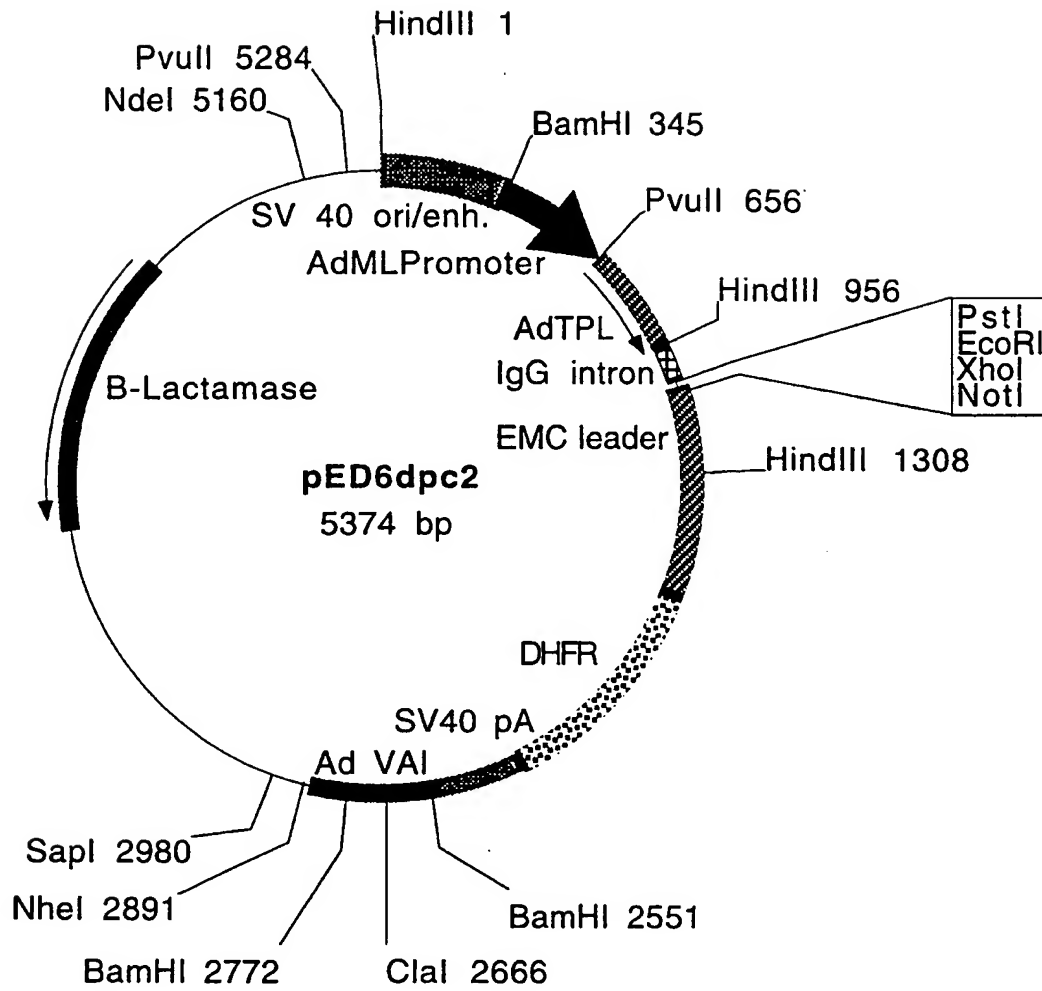
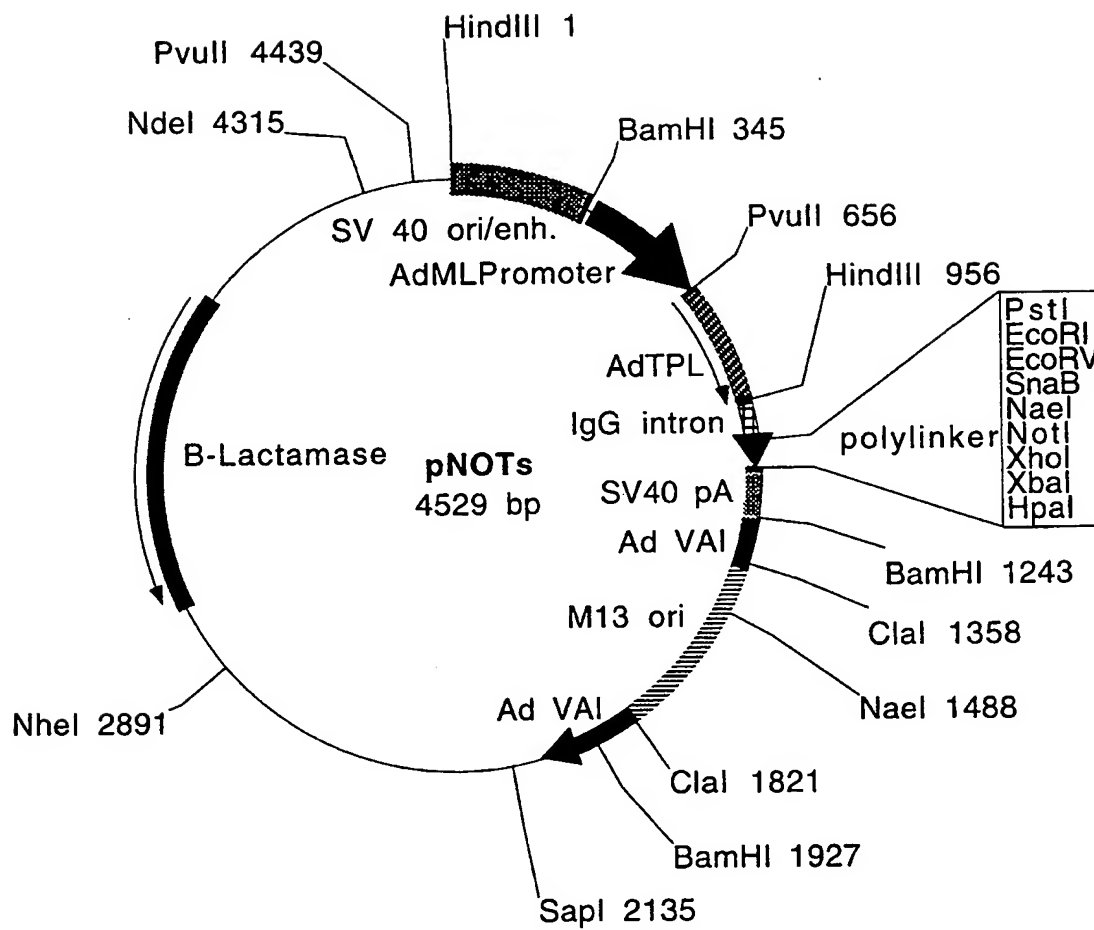


Fig. 1B



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 Hoffman, Heidi
 Hall, Jeff
 Rapiejko, Peter

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<210> 2

<211> 78

<212> PRT

<213> Homo sapiens

<400> 2

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Met Val Leu Thr Leu Trp Cys Asn Leu Cys Ser Arg Ala Ser Ser Trp
  1             5             10            15

```

```

Val Arg Gln Lys His Val Ser Cys Cys Val His Asn Tyr Thr Gln Pro
          20             25             30

```

```

Phe Leu Leu Ile Gln Ser Ser Phe Trp Ala Met Ser Ser Glu Thr Lys
  35             40             45

```

```

Pro Lys Ala Leu Ser Lys Asp Tyr Leu Cys Ile Ser Tyr Arg Ser Pro
  50             55             60

```

```

His Ser Thr Pro Thr His Arg His Ser Ser Asn Arg Phe Leu
  65             70             75

```

<210> 3

<211> 1326

<212> DNA

<213> Homo sapiens

<400> 3

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1326

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<210> 4

<211> 440

<212> PRT

<213> Homo sapiens

<400> 4

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Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu
  1              5              10              15

Trp Gly Gln Arg Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly
      20              25              30

Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln
      35              40              45

Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu
      50              55              60

Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu
      65              70              75              80

Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr
      85              90              95

Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser
      100             105             110

Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val
      115             120             125

Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu
      130             135             140

```

Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val
 145 150 155 160
 Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys
 165 170 175
 Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu
 180 185 190
 Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His
 195 200 205
 Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe
 210 215 220
 His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp Ile
 225 230 235 240
 Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala Ala
 245 250 255
 Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe Leu
 260 265 270
 Ala Ala Gly Ser Gly Cys Thr Ser Ser Trp Trp Arg Ala Pro Pro Cys
 275 280 285
 Leu Leu Arg Ala His Gly Leu Gln Val Pro Ala His Arg Lys Gln Pro
 290 295 300
 Val Pro Ala Ala Ala Pro Gly Gly Arg Gly Gly Cys Ser Asp Gly Ala
 305 310 315 320
 Ser Asn Asp Gly Leu Trp Val Pro Gly Arg Pro Leu Gln Ser Gln Gln
 325 330 335
 Asn Ser Gln Arg Ala Gly Thr Val Met Ile Thr Ser Thr Ser Gln Thr
 340 345 350
 Lys Gly Ser Ser Ser Pro Ser Ile Ser His Ser Cys Pro Ser Ser Thr
 355 360 365
 Ala Tyr Val Gly Arg Trp Arg Gly Ser Met Trp Thr Arg Arg Pro Ala
 370 375 380
 Pro Arg Asp Pro Gly Ser Arg Thr Ser Pro Phe Gly Arg Arg Val Pro
 385 390 395 400
 Ser Ser Pro Gln Ile Leu Gly Ser Pro Val Leu Thr Pro Gly Pro Pro
 405 410 415
 Leu Pro Ser Ser Tyr Val Tyr Asn Asn Asp Gln Ser Val Trp Leu Lys
 420 425 430
 Lys Lys Lys Lys Lys Lys Lys Lys
 435 440

<210> 5

<211> 1280
 <212> DNA
 <213> Homo sapiens

<400> 5
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 tagtcacctg aggatttttg gagacagaat ggagaatgaa ttgattgcct tgggtgcctc 180
 attcagggat gtgacagcag ctagtacaca ctgcatttgt gataaggctg atacgagggg 240
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 aaagaaatag ctggacagtc cagaagctat ctggctcaga catccattta tctcaggctg 600
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 aattagccag gcgtgggtggc gggcgctgt agtcccagct acttgggagg ctgaggcagc 960
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<210> 6
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 6
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 Arg Gly Tyr Val Phe Leu Lys Met Tyr Leu Val Lys Glu Lys Asn Pro
 35 40 45
 Leu Phe Ile Tyr Asp Gly Lys Leu Gly Thr
 50 55

<210> 7
 <211> 1001
 <212> DNA
 <213> Homo sapiens

<400> 7
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 cctcacaggc ttcacagggc agaagtgtga gactgatgtc aatgagtggt acattccagg 420

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ggaatggaaa agaacacgat gagaattaga cactggaaaa tatgtatgtg tggttaataa 960
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1001

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<210> 8
 <211> 114
 <212> PRT
 <213> Homo sapiens

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<400> 8
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Trp Pro Thr Ser Ser Pro Ala Asn Ala Ser Gln Ala Ser Gln Gly Arg
          20             25             30
Ser Val Arg Leu Met Ser Met Ser Val Thr Phe Gln Asp Thr Ala Ser
      35             40             45
Met Val Ala Pro Ala Ser Thr Cys Leu Val Pro Thr Ser Ala Ser Ala
      50             55             60
Phe Arg Ala Ser Gln Ala Ser Thr Val Thr Ala Cys Met Cys Pro Val
      65             70             75             80
His Pro Arg Leu Val Ser Met Glu Ala Pro Val Gly Arg Leu Val Thr
          85             90             95
Ser Leu Leu Ser Ala Thr Ala Phe Gln Val Arg Ser Ser Leu Val Ser
      100             105             110
Gln Asp

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<210> 9
 <211> 2058
 <212> DNA
 <213> Homo sapiens

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<400> 9
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ctcatctgta gtttccaaga gttcagctga agcagatgga gtcttcgagc ccaggagaca 180
ccctgcatcc ctgctaatag tgtttgccac aagtattagt gactcttcct tattaatatt 240
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ccaggctgag tgagatgagc tgcagctggc tcatggcctt cttagagcag agagaggagt 660
atgtcatttt actaagttcc taaacaaaca tttatgcagg caacactcct tgcagatcca 720

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```

gaaactgagg cacaataggg ttatgacttg ctcaagaata tgtagctgct aggggggtaaa 780
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cccaaagtct accactgtta atcttttggg gttaaattgt cccctagac atttctgtgc 1920
atagattttt ggtgtgttta catagtcgtt attctgtata tacaatttta tgtccctttt 1980
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aaaaaaaaaa aaaaaaaaaa                                     2058

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<210> 10

<211> 96

<212> PRT

<213> Homo sapiens

<400> 10

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Met Thr Phe Asp Phe Cys Cys Leu Tyr Phe Ser Thr Val Tyr Ala Pro
  1             5             10             15

Ser Phe Lys Tyr Ile Cys Val His Thr Asp Thr His Ile Cys Val Cys
          20             25             30

Val Cys Ile Tyr Leu Ser Ser Val Val Ser Lys Ser Ser Ala Glu Ala
          35             40             45

Asp Gly Val Leu Gln Pro Arg Arg His Pro Ala Ser Leu Leu Ile Val
          50             55             60

Phe Ala Thr Ser Ile Ser Glu Ser Ser Leu Leu Ile Phe Ser Phe Gln
          65             70             75             80

Lys Thr Glu Ala Lys Leu Ile Val Phe Ala Val Ser Leu Ala Ala Lys
          85             90             95

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<210> 11

<211> 1498

<212> DNA

<213> Homo sapiens

<400> 11

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tcttcttccc tgaagagagg tgggcctgag gcttgacagt ggcgctgcct gagtgcacta 180
gccgctgggc tgggccctgg acagctgac ccaggttctt gcaactgtcg ccacccttcc 240
gtagtcacac ggcctgatgg cggcggcggc tgagccgatg ggcccgac aggttcccat 300

```

```

gaactcagaa gtaattgtgg accctataca ggggcaggtg aactttgagg acgtgttcgt 360
gtacttctcc caggaggagt ggggtctcct tgatgaggct cagaggctcc tgtaccgtga 420
tgtgatgctg gagaactttg cacttatggc ctctctgggg atacctcaga caatggcagc 480
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aataccagag ctaaaaatga aagtcattga tactgttaca caaagaacac tctatataac 1020
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ttgggaggct gaggcactcc caaatgcctc aagtgtacca ctcaagatga cttgaggcca 1320
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caaccatgtg gcacacacct gtagtcccag ctactccaga gggatgaagc cgagaattac 1440
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<210> 12

<211> 117

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Ala Ala Ala Glu Pro Met Gly Pro Ala Gln Val Pro Met Asn
  1             5             10             15

```

```

Ser Glu Val Ile Val Asp Pro Ile Gln Gly Gln Val Asn Phe Glu Asp
      20             25             30

```

```

Val Phe Val Tyr Phe Ser Gln Glu Glu Trp Val Leu Leu Asp Glu Ala
    35             40             45

```

```

Gln Arg Leu Leu Tyr Arg Asp Val Met Leu Glu Asn Phe Ala Leu Met
    50             55             60

```

```

Ala Ser Leu Gly Ile Pro Gln Thr Met Ala Ala Phe Gly Leu Lys Tyr
    65             70             75             80

```

```

Leu Leu Asn Asp Thr Gly Tyr Thr Ser Ser Lys Ser Asn Thr Ile Thr
    85             90             95

```

```

Ala Thr Asp Ser Pro Ala Asp Leu Pro Arg Lys Thr Glu Pro His Thr
   100             105             110

```

```

Pro Ser Trp Ser Trp
   115

```

<210> 13

<211> 1718

<212> DNA

<213> Homo sapiens

<400> 13

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```



```

ccccgaccgct gccggccgcg ctcccgtgc tcttgccggg tgatggaaaa ccccgagccg 180
gccgcccggcc tgggcaaggc cctctgcgct ctctctctgg ccactctcgg cgccgcccggc 240
cagcctcttg ggggagagtc catctgttcc gccggagccc cggccaaata cagcatcacc 300
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<210> 14

<211> 105

<212> PRT

<213> Homo sapiens

<400> 14

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Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala
  1             5             10             15

Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu
      20             25             30

Ser Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr
      35             40             45

Gly Lys Trp Ser Gln Thr Ala Ser Pro Ser Ser Thr Pro Cys Ser Ala
      50             55             60

Pro Leu Arg Ser Gly Leu Arg Cys Trp Gly Pro Arg Ile Ala Pro Thr
      65             70             75             80

Thr Ala Cys Gly Gly Arg Thr Ser Thr Ser Val Thr Gly Cys Ala Thr
      85             90             95

Leu Arg Ser Ala Ala Arg Pro Gly Arg
      100             105

```

<210> 15

<211> 847

<212> DNA

<213> Homo sapiens

<400> 15

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 ggggacaggg cgccactcac agccacagcc ccacaactgg atgatgagga gatgtactca 180
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 ctctgtgctg ccacctctgc tccctcctcc agcctcaggg cactcggggc tgggtgggag 780
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<210> 16

<211> 189

<212> PRT

<213> Homo sapiens

<400> 16

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 20 25 30
 Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
 35 40 45
 Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
 50 55 60
 Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
 65 70 75 80
 Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser
 85 90 95
 Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
 100 105 110
 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
 115 120 125
 Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
 130 135 140
 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
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 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
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 Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
 180 185

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 <211> 1448
 <212> DNA
 <213> Homo sapiens

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 aaaaaaaaaa 1448

<210> 18
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 18
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 20 25 30
 Ser Leu His Phe Pro Ser Ser Ser Asp Ser Pro Ala Ser Ala Ser Arg
 35 40 45
 Val Ala Gly Thr Thr Gly Ala Cys His His Ala Arg Leu Ile Phe Val
 50 55 60
 Phe Leu Val Glu Thr Glu Phe His Cys Val Gly Gln Asp Gly Leu Asp
 65 70 75 80
 Leu Asp Leu Val Ile Thr His Leu Gly Leu Ser Lys Cys Trp Asp Tyr
 85 90 95
 Arg Arg Glu Pro Pro Arg Leu Ala Tyr Val
 100 105

<210> 19
 <211> 2166
 <212> DNA
 <213> Homo sapiens

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<210> 20
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 20
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 20 25 30
 Trp Val Leu Thr Leu Thr Ala Glu Ser Gly Leu Ala Arg Thr Gln Ser
 35 40 45

Lys Ser Val Phe Gln Leu Ser Ile Ser Leu Val Glu
50 55 60

<210> 21
<211> 1833
<212> DNA
<213> Homo sapiens

<400> 21
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gagggattgt tttagcagct cctctccaga gggggctgga agtccagttt caccaatgac 180
caagttttat ttccttggtc ttgttttagt ttttccattt tgttttcagt ccagggtgct 240
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<210> 22
<211> 55
<212> PRT
<213> Homo sapiens

<400> 22
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Phe Gln Ser Arg Cys Leu Ala Ala Leu Leu Glu Trp Ala Ser Ile Ser
20 25 30

Leu Ile Leu Ser Ala Met Cys Phe Val Pro Leu Gln Thr Cys Phe Leu
35 40 45

Phe Leu Leu Ala Val Ala Leu
50 55

<210> 23
 <211> 1504
 <212> DNA
 <213> Homo sapiens

<400> 23
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 cactggagga gtgactttgt cggtcattgc atccccagtt attgctgcag ttagtggttg 180
 tattggtgtc cccattatgc tggcatatgt ttatgggggt gtgcccattt ctctttgtcg 240
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 aaaa 1504

<210> 24
 <211> 361
 <212> PRT
 <213> Homo sapiens

<400> 24
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 35 40 45
 Ser Val Gly Ile Gly Val Pro Ile Met Leu Ala Tyr Val Tyr Gly Val
 50 55 60
 Val Pro Ile Ser Leu Cys Arg Gly Gly Gly Cys Gly Val Ser Thr Ala
 65 70 75 80
 Asn Gly Lys Gly Val Lys Ile Glu Phe Asp Glu Asp Asp Gly Pro Ile
 85 90 95
 Thr Val Ala Asp Ala Trp Arg Ala Leu Lys Asn Pro Ser Ile Gly Glu
 100 105 110

Ser Ser Ile Glu Gly Leu Thr Ser Val Leu Ser Thr Ser Gly Ser Pro
 115 120 125
 Thr Asp Gly Leu Ser Val Met Gln Gly Pro Tyr Ser Glu Thr Ala Ser
 130 135 140
 Phe Ala Ala Leu Ser Gly Gly Thr Leu Ser Gly Gly Ile Leu Ser Ser
 145 150 155 160
 Gly Lys Gly Lys Tyr Ser Arg Leu Glu Val Gln Ala Asp Val Gln Lys
 165 170 175
 Glu Ile Phe Pro Lys Asp Thr Ala Ser Leu Gly Ala Ile Ser Asp Asn
 180 185 190
 Ala Ser Thr Arg Ala Met Ala Gly Ser Ile Ile Ser Ser Tyr Asn Pro
 195 200 205
 Gln Asp Arg Glu Cys Asn Asn Met Glu Ile Gln Val Asp Ile Glu Ala
 210 215 220
 Lys Pro Ser His Tyr Gln Leu Val Ser Gly Ser Ser Thr Glu Asp Ser
 225 230 235 240
 Leu His Val His Ala Gln Met Ala Glu Asn Glu Glu Glu Gly Ser Gly
 245 250 255
 Gly Gly Gly Ser Glu Glu Asp Pro Pro Cys Arg His Gln Ser Cys Glu
 260 265 270
 Gln Lys Asp Cys Leu Ala Ser Lys Pro Trp Asp Ile Ser Leu Ala Gln
 275 280 285
 Pro Glu Ser Ile Arg Ser Asp Leu Glu Ser Ser Asp Ala Gln Ser Asp
 290 295 300
 Asp Val Pro Asp Ile Thr Ser Asp Glu Cys Gly Ser Pro Arg Ser His
 305 310 315 320
 Thr Ala Ala Cys Pro Ser Thr Pro Arg Ala Gln Gly Ala Pro Ser Pro
 325 330 335
 Ser Ala His Met Asn Leu Ser Ala Leu Ala Glu Gly Gln Thr Val Leu
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<210> 25

<211> 2350

<212> DNA

<213> Homo sapiens

<400> 25

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<210> 26

<211> 167

<212> PRT

<213> Homo sapiens

<400> 26

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Met Tyr His Gln Leu Leu Lys Phe Leu Ile Ile Gly His Leu Lys Leu
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Leu Arg Asp Phe Asp Phe Leu Gly Glu Asp Gly Val Cys His Leu Leu
      20             25             30

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Ala Thr Ile Ile Ala Leu Ser Gln Ile Gln Lys Ile Leu Thr Lys Asn
      35             40             45

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Leu Lys Val Glu Ile Gln Asp His Gly Tyr Leu Pro His Leu Glu Ile
      50             55             60

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Asp Ala His Leu Cys Ser Leu Glu Gly Gly Glu Arg Glu Glu Met Asn
      65             70             75             80

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Leu Gln Gly Tyr Leu Pro Leu Ile His His Leu Asp Leu Ile Phe Leu
      85             90             95

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Glu Glu Asn Gln Met Lys Trp Phe Thr Leu Lys His Arg Met Ile Leu
 100 105 110
 Leu Glu Leu Leu Pro Thr Asp His Lys His Leu Gln His Gln Ala Val
 115 120 125
 Pro Gln Gln Val Ala Leu His Gln Ile Arg Leu Lys Val Glu Glu Ile
 130 135 140
 Gln Glu Tyr Gln Gly Phe Phe Leu Val Pro Tyr Ser Gly Leu Gln Ser
 145 150 155 160
 Pro Gln His Leu Gly Val Ile
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<210> 27
 <211> 1635
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Lys Pro Gln Gly Ile Arg Gly Leu Val Leu Gln His Pro Val Leu
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<210> 29

<211> 3415

<212> DNA

<213> Homo sapiens

<400> 29

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<210> 30

<211> 55

<212> PRT

<213> Homo sapiens

<400> 30

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Ser Ser Trp Val Asn Gly Asp Cys Gly Ser Cys Leu Ser Ile Ser Asp
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Ser Ser Asn Asp Thr Gly Lys
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<210> 31

<211> 2967

<212> DNA

<213> Homo sapiens

<400> 31

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<210> 32

<211> 250

<212> PRT

<213> Homo sapiens

<400> 32

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Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20                      25                      30

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Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35                      40                      45

```

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Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50                      55                      60

```

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Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65                      70                      75                      80

```

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Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85                      90                      95

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Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
 100 105 110
 Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
 115 120 125
 Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
 130 135 140
 Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
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<210> 33

<211> 2926

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 55

<212> PRT

<213> Homo sapiens

<400> 34

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Ile Ser Leu Leu Ala Val Gly Thr Asp Ser Asp Gly Asn Val Ala Thr
          20                      25                      30

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Glu Cys Phe Leu Ser Phe Leu Val Pro Ser Ile Phe Ile Ser Thr Phe
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Leu Val Cys Cys Pro Leu Phe
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<210> 35

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 35

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<210> 36

<211> 79

<212> PRT

<213> Homo sapiens

<400> 36

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    20             25             30

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Tyr Phe Ser Glu Lys Val His Pro Phe Leu Val Leu Arg Thr Ile Lys
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Ile His Tyr Asp Glu Leu Tyr Leu Ile Tyr Val Tyr Phe Asp Thr Gly
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Phe Lys Glu His Leu Arg Glu Glu Cys Ser Leu Asp Leu Leu Asn
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<210> 37

<211> 2248

<212> DNA

<213> Homo sapiens

<400> 37

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<210> 38

<211> 119

<212> PRT

<213> Homo sapiens

<400> 38

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 35 40 45

Tyr Phe His Cys Thr Leu Ile Gly Tyr Phe Val Gly Leu Leu Thr Ala
 50 55 60

Thr Val Ala Ser Arg Ile His Arg Ala Ala Gln Pro Ala Leu Leu Tyr
 65 70 75 80

Leu Val Pro Phe Thr Leu Leu Pro Leu Leu Thr Met Ala Tyr Leu Lys
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Gly Asp Leu Arg Arg Met Trp Ser Glu Pro Phe His Ser Lys Ser Ser
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Ser Ser Arg Phe Leu Glu Val
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<210> 39

<211> 931

<212> DNA

<213> Homo sapiens

<400> 39

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<211> 53

<212> PRT

<213> Homo sapiens

<400> 40

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Ala Val Thr Ser Leu Thr Thr Leu Ile Ser Gln Pro Cys Leu Phe Phe

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25

30

Leu Thr Leu Ser Pro Pro Pro Leu Arg Arg His Cys Arg Gly Pro Pro
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Gly Arg Arg Leu Ser
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<211> 3625

<212> DNA

<213> Homo sapiens

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<210> 42

<211> 488

<212> PRT

<213> Homo sapiens

<400> 42

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Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His
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Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val
          50                      55                      60

Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro
          65                      70                      75                      80

Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln
          85                      90                      95

Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp
          100                      105                      110

Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr
          115                      120                      125

Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys
          130                      135                      140

Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala
          145                      150                      155                      160

Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser
          165                      170                      175

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| Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu | | |
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| Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr | | |
| | 275 | 280 285 |
| His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu | | |
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| Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu | | |
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| Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys | | |
| | 325 | 330 335 |
| Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu | | |
| | 340 | 345 350 |
| Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe | | |
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| Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro | | |
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| Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala Ala Ala Gln Thr | | |
| | 385 | 390 395 400 |
| Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys | | |
| | 405 | 410 415 |
| Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile | | |
| | 420 | 425 430 |
| Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His | | |
| | 435 | 440 445 |
| Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu | | |
| | 450 | 455 460 |
| Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu | | |
| | 465 | 470 475 480 |
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<210> 43

<211> 2861

<212> DNA

<213> Homo sapiens

<400> 43

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<210> 44

<211> 84

<212> PRT

<213> Homo sapiens

<400> 44

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Met Lys Phe His Ile Lys Asn Asp Asp Lys Phe Thr His Cys Ala Ile
1           5           10          15

```

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 20 25 30

Ser Glu His Trp Asp Asn Trp Ser Phe Lys Asn Ile His Pro Leu Thr
 35 40 45

Ala Ser Leu Ser Gly Tyr Phe Tyr Leu Cys Val Gln Arg His Phe Phe
 50 55 60

Ser Ala Val Ile Ile Ile Thr Ser Gln Lys Lys Met Leu Thr Asp Leu
 65 70 75 80

Leu Thr Gly Pro

<210> 45
 <211> 1556
 <212> DNA
 <213> Homo sapiens

<400> 45
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<210> 46
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 46
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 Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu Val Tyr
 35 40 45
 Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys Leu Leu
 50 55 60
 His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val Gly Leu
 65 70 75 80
 Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn Leu Tyr
 85 90 95
 Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe Ala Cys
 100 105 110
 Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala Ser Met
 115 120 125
 Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly Ala Ala
 130 135 140
 Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn Glu Lys
 145 150 155 160
 Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser Leu Pro
 165 170 175
 Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val Ala Phe
 180 185 190
 Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys Arg Pro
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 210 215 220

<210> 47

<211> 2446

<212> DNA

<213> Homo sapiens

<400> 47

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<210> 48

<211> 74

<212> PRT

<213> Homo sapiens

<400> 48

```

Met Thr Glu Gly Ile Phe Thr Leu Gly Ser Leu Leu Glu Leu Gln Cys
  1                      5                      10                      15

```

```

Pro Gly Arg Gly Glu Glu Lys Pro Asp Leu Glu His Ser Ser Ser Leu
          20                      25                      30

```

```

His Ser Pro Leu Leu Ser Gln Ala Leu Gly Cys Gly Phe Ile Phe Pro
          35                      40                      45

```

```

Ser Ser Leu Thr Thr Gln Glu Ala Gln Ser Phe Ser Leu Lys Lys Gly
          50                      55                      60

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Gly Pro Ala Leu Phe Pro Leu Leu Gln Asn
  65                      70

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<210> 49

<211> 1231

<212> DNA

<213> Homo sapiens

<400> 49

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acatcacgcg cttcatcgcc tgctctcgcg cagttgacct gacatccctg agggggaccc 240
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<210> 50

<211> 113

<212> PRT

<213> Homo sapiens

<400> 50

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Met Phe Val Ala Val Phe Leu Trp Leu Val Thr Ile Val Leu Phe Asn
  1              5              10             15

Leu Tyr Leu Phe Gln Leu His Met Lys Leu Tyr Met Val Pro Trp Pro
          20              25             30

Leu Val Leu Met Ile Phe Asn Ile Ser Ala Thr Val Leu Tyr Ile Thr
          35              40             45

Ala Phe Ile Ala Cys Ser Ala Ala Val Asp Leu Thr Ser Leu Arg Gly
          50              55             60

Thr Arg Pro Tyr Asn Gln Arg Ala Ala Ala Ser Phe Phe Ala Cys Leu
          65              70             75             80

Val Met Ile Ala Tyr Gly Val Ser Ala Phe Phe Ser Tyr Gln Ala Trp
          85              90             95

Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln Met Ala Gly Gly Tyr
          100             105            110

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Ala

<210> 51

<211> 3290

<212> DNA

<213> Homo sapiens

<400> 51

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<210> 52

<211> 518

<212> PRT

<213> Homo sapiens

<400> 52

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Met Pro Val Ser Pro Leu Ala Val Ala Ala Met Leu Ala Cys Ala Arg
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Ile Gly Ala Val His Thr Val Ile Phe Ala Gly Phe Ser Ala Glu Ser

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ala | Gly | Arg | Ile | Asn | Asp | Ala | Lys | Cys | Lys | Val | Val | Ile | Thr | Phe | |
| 35 | | | | | 40 | | | | | 45 | | | | | | |
| Asn | Gln | Gly | Leu | Arg | Gly | Gly | Arg | Val | Val | Glu | Leu | Lys | Lys | Ile | Val | |
| 50 | | | | | 55 | | | | | 60 | | | | | | |
| Asp | Glu | Ala | Val | Lys | His | Cys | Pro | Thr | Val | Gln | His | Val | Leu | Val | Ala | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| His | Arg | Thr | Asp | Asn | Lys | Val | His | Met | Gly | Asp | Leu | Asp | Val | Pro | Leu | |
| 85 | | | | | 90 | | | | | 95 | | | | | | |
| Glu | Gln | Glu | Met | Ala | Lys | Glu | Asp | Pro | Val | Cys | Ala | Pro | Glu | Ser | Met | |
| 100 | | | | | 105 | | | | | 110 | | | | | | |
| Gly | Ser | Glu | Asp | Met | Leu | Phe | Met | Leu | Tyr | Thr | Ser | Gly | Ser | Thr | Gly | |
| 115 | | | | | 120 | | | | | 125 | | | | | | |
| Met | Pro | Lys | Gly | Ile | Val | His | Thr | Gln | Ala | Gly | Tyr | Leu | Leu | Tyr | Ala | |
| 130 | | | | | 135 | | | | | 140 | | | | | | |
| Ala | Leu | Thr | His | Lys | Leu | Val | Phe | Asp | His | Gln | Pro | Gly | Asp | Ile | Phe | |
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| Gly | Cys | Val | Ala | Asp | Ile | Gly | Trp | Ile | Thr | Gly | His | Ser | Tyr | Val | Val | |
| 165 | | | | | 170 | | | | | 175 | | | | | | |
| Tyr | Gly | Pro | Leu | Cys | Asn | Gly | Ala | Thr | Ser | Val | Leu | Phe | Glu | Ser | Thr | |
| 180 | | | | | 185 | | | | | 190 | | | | | | |
| Pro | Val | Tyr | Pro | Asn | Ala | Gly | Arg | Tyr | Trp | Glu | Thr | Val | Glu | Arg | Leu | |
| 195 | | | | | 200 | | | | | 205 | | | | | | |
| Lys | Ile | Asn | Gln | Phe | Tyr | Gly | Ala | Pro | Thr | Ala | Val | Arg | Leu | Leu | Leu | |
| 210 | | | | | 215 | | | | | 220 | | | | | | |
| Lys | Tyr | Gly | Asp | Ala | Trp | Val | Lys | Lys | Tyr | Asp | Arg | Ser | Ser | Leu | Arg | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Thr | Leu | Gly | Ser | Val | Gly | Glu | Pro | Ile | Asn | Cys | Glu | Ala | Trp | Glu | Trp | |
| 245 | | | | | 250 | | | | | 255 | | | | | | |
| Leu | His | Arg | Val | Val | Gly | Asp | Ser | Arg | Cys | Thr | Leu | Val | Asp | Thr | Trp | |
| 260 | | | | | 265 | | | | | 270 | | | | | | |
| Trp | Gln | Thr | Glu | Thr | Gly | Gly | Ile | Cys | Ile | Ala | Pro | Arg | Pro | Ser | Glu | |
| 275 | | | | | 280 | | | | | 285 | | | | | | |
| Glu | Gly | Ala | Glu | Ile | Leu | Pro | Ala | Met | Ala | Met | Arg | Pro | Phe | Phe | Gly | |
| 290 | | | | | 295 | | | | | 300 | | | | | | |
| Ile | Val | Pro | Val | Leu | Met | Asp | Glu | Lys | Gly | Ser | Val | Val | Glu | Gly | Ser | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Asn | Val | Ser | Gly | Ala | Leu | Cys | Ile | Ser | Gln | Ala | Trp | Pro | Gly | Met | Ala | |
| 325 | | | | | 330 | | | | | 335 | | | | | | |
| Arg | Thr | Ile | Tyr | Gly | Asp | His | Gln | Arg | Phe | Val | Asp | Ala | Tyr | Phe | Lys | |

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<210> 53
<211> 1467
<212> DNA
<213> Homo sapiens

<400> 53
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taactgttgc agtgaaagtg caatatctga cccccctgct ccagcagga agttgcttgg 540
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<210> 54
 <211> 132
 <212> PRT
 <213> Homo sapiens

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<400> 54
Met Tyr Lys Ala Thr Ile Ile Leu Trp Thr Lys Phe Ser Cys Asn Cys
  1             5             10             15
Cys Ser Glu Ser Ala Ile Ser Asp Pro Pro Ala Pro Ser Arg Lys Leu
          20             25             30
Leu Gly Pro Thr Ile Thr Ala Pro Val Arg Gly Pro Val Ala Ser Ala
      35             40             45
Ser Ser Ser Leu Gly Pro Thr Leu Ser Cys Leu Ala Cys Cys Leu Gly
      50             55             60
Asp Gln Pro Ser Arg Glu Ala Pro Gly Arg Val Ser Gly Pro Pro Ala
      65             70             75             80
Ile Lys Ala Gly Arg Pro Cys Gly Gln Trp Ala Gln Pro Leu Pro Arg
          85             90             95
Gly Ala Ala Pro Pro Arg Leu Leu Thr Pro Arg Leu Pro Ala Gln Pro
      100             105             110
Pro Ala Met Pro Arg Thr Thr Ala Ile Val Pro Trp Gly Ser Pro Ser
      115             120             125
Gly Pro Gln Pro
      130

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<210> 55
 <211> 943
 <212> DNA
 <213> Homo sapiens

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<400> 55
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ctttggttct ctttgtattt actacttttc tctttttctt gtgttttttt ttctctgttt 180
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cgcagacgat atctctctcg gcctcttaat cccttacctg agaatgaagg gatttaaaac 420
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tacaaccaga atacagtgtt tggaaacctaa atctgtttgt gcgtctgcat caaaggaaca 600
tttgcttcac tgggtgataa cctttgatga aatgagatat gtccaagtaa cgtaactgt 660
gaagttacac acagtagctg acttcaaagt gcctgttctg taaattttat tttaaactgt 720

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 943

<210> 56
 <211> 86
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Asn Ile Leu Lys Leu Phe Phe Phe Phe Leu Ala Cys Val Phe Ser
 1 5 10 15
 Ser Leu Val Leu Phe Val Phe Thr Thr Phe Leu Phe Phe Leu Cys Phe
 20 25 30
 Phe Phe Pro Val Phe Val Leu Phe Gly Val Leu Phe Leu Ser Ser Leu
 35 40 45
 Phe Gln Val Phe Leu Tyr Pro Ser Gly Phe Pro Thr Gly Trp Ile Glu
 50 55 60
 Met Val Gln Leu Cys Pro Ala Pro Ser Ser Ser Ser Ser Ser Gly
 65 70 75 80
 Arg Ala Leu Leu Arg Cys
 85

<210> 57
 <211> 1032
 <212> DNA
 <213> Homo sapiens

<400> 57
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 agcgctagtt cataatttaa aaaaatttaa aaaacgcaac agccaacttt tcttaatacc 180
 atataccttt taaaacacag tggcaggtaa taagtgggaag agaagaatgt ttctgtctct 240
 tcctacgttg actgttctta ttccactggt ttcttttagca ggactgttct actcagcctc 300
 tgtggaagaa aacttcccac agggctgcac tagcacagcc agcctttgct ttacagcct 360
 gctcttgcct attaccatac cagtgtatgt attcttccac ctttggactt ggatgggtat 420
 taaactcttc aggcataatt gatgcaacta gagtcaatat gctgtatata ttaatgatag 480
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 attgtactct tgttctgccc ttgttttttg aaggctctga cttataactg ctgtatcaga 660
 agaaacattt tgacagtgtc ttggttggag atgaacatcc ctaattgaca tgtgatgact 720
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 caaggctctt ggtaaagtca catgttaagg atgactgaaa taattccaaa ggagtgatgt 840
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 atcaaataga aacttcatgt acttacaaaa actgagtttg taaaattacc ttcatcttct 960
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<210> 58
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 58

Met Phe Leu Ser Leu Pro Thr Leu Thr Val Leu Ile Pro Leu Val Ser
 1 5 10 15

Leu Ala Gly Leu Phe Tyr Ser Ala Ser Val Glu Glu Asn Phe Pro Gln
 20 25 30

Gly Cys Thr Ser Thr Ala Ser Leu Cys Phe Tyr Ser Leu Leu Leu Pro
 35 40 45

Ile Thr Ile Pro Val Tyr Val Phe Phe His Leu Trp Thr Trp Met Gly
 50 55 60

Ile Lys Leu Phe Arg His Asn
 65 70

<210> 59

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 59

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 tggaaattaa aaggcacctt ttactgcatt ctctctgtgc tttgtctagg tcctttctag 180
 agccttcagg aatcggtttg tggaattgca ctttgatgag ttacctagct ccgagttgga 240
 aacaatcttg cacaagcggg gtagtttgcc accctcctat tgcagcaagt tgggttaaagt 300
 catgctggat cttcaggtag ttagtttcaa atggaatgta ttgattatac ttggtgatca 360
 aaatttcatg gcttcttttg ttagaaaaaa gaatctgtct gttgatgat ttttccaagt 420
 agagattttt ttttattttt tattgttttt aattttttta ttattttatt tttgcaagac 480
 acagtctcac tctactctcc tggctggagt gtagtggcac aatcatagct cattgcagcc 540
 ttgacctcct gggctcagg gatcctccca tctctgacta ctactcctt agtagctggg 600
 accacagatg tgcaccgtca tggccgggta catttttttt tttgtagaga caaggtttcg 660
 ccatgttgcc ccggctggg tgcgaactcct gggctcaagg gatccacca ccttgatctc 720
 ccaaagtttt gggattatag gtgtgaacca cagtctcttg ccttcaagta gaggtctttt 780
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 aaaa 1564

<210> 60

<211> 82

<212> PRT

<213> Homo sapiens

<400> 60

Met Val Asn Val Arg Ala Ser Ile Leu Glu Ile Lys Arg His Leu Leu
 1 5 10 15

Leu His Ser Ser Cys Ala Leu Ser Arg Ser Phe Leu Glu Pro Ser Gly
 20 25 30
 Ile Gly Leu Trp Asn Cys Thr Leu Met Ser Tyr Leu Ala Pro Ser Trp
 35 40 45
 Lys Gln Ser Cys Thr Ser Gly Val Val Cys His Pro Pro Ile Ala Ala
 50 55 60
 Ser Trp Leu Lys Ser Cys Trp Ile Phe Arg Tyr Leu Val Ser Asn Gly
 65 70 75 80
 Met Tyr.

<210> 61

<211> 2800

<212> DNA

<213> Homo sapiens

<400> 61

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 ttagaattgg ttttgttttt attctattat cttttatttc cagttgtcaa actttaaatg 180
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 aaatgttgct cagggtctgt gtcagtgaga aaaatttatt aatgcttttt aatgtgtttt 300
 tacccttgcc tcaactctgt tgtgtcactt tctataatat aaagaaatac tataatattt 360
 ctagaatctg gaactgtcac catgatgaat ggccctttca atgcatagtt acagaaattc 420
 ctgaagattc cccaggactt caatttcatt ggtttttatt tgcagttttt agttgctgta 480
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 agaactcctt ttgattttgc ttttctctgc ccctagaaat tttagggaca aagacatttt 660
 ggaaattgtc agttactttt agaaagaaaa cactgcagaa atatttaaca gattacttct 720
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 aattttaaaaa cccagcactt gataatataa ctgacagaaa tgattgtacc cactgatgaa 2160
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<210> 62

<211> 170

<212> PRT

<213> Homo sapiens

<400> 62

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Met Phe Ser Cys Asn Glu Asn Ser Ile Phe Phe Arg Ile Gly Phe Val
  1             5             10             15

Phe Ile Leu Leu Ser Phe Ile Ser Ser Cys Gln Thr Leu Asn Gly Tyr
          20             25             30

Val Cys Ile Leu Ile Thr Leu Phe Ser Leu Leu Trp Lys Arg Arg Thr
          35             40             45

Arg Glu Gln Met Leu Leu Arg Ala Gly Val Ser Glu Lys Asn Leu Ser
          50             55             60

Met Leu Phe Asn Val Phe Leu Pro Leu Pro His Ser Val Cys Val Thr
          65             70             75             80

Phe Tyr Asn Ile Lys Lys Tyr Tyr Asn Ile Ser Arg Ile Trp Asn Cys
          85             90             95

His His Asp Glu Trp Pro Phe Gln Cys Ile Val Thr Glu Ile Pro Glu
          100            105            110

Asp Ser Pro Gly Leu Gln Phe His Trp Phe Leu Phe Ala Val Phe Ser
          115            120            125

Cys Cys Asn Cys Cys Cys Phe Gln Ser Lys Gly Pro Pro Leu Val Lys
          130            135            140

Val Asn Lys Thr Ser Pro Leu Cys Tyr Pro Ala Arg Phe Cys Val Cys
          145            150            155            160

Asn Gly Leu Ala Gln Glu Cys Ser Phe Thr
          165            170

```

<210> 63

<211> 2056

<212> DNA

<213> Homo sapiens

<400> 63

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tgcaaaactca cgctcgagcc agttttgctg cagggccttc tcagaagact tctcagccca 120
tttggtccag gatcaacaca gccagaagt gcaggggcat taccagcca ggggcaatcc 180
tccagcagtg ggagatacaa gcctatggat gaaggttccc acctcccatc actcagatga 240

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ctttgacaca gacgaatatt gccttaatgc tttctcattg cagctccatt ctcatctc 1920
ttgttcta at ctcactggga acagtaagaa gctgccatca ttttatgtta tacttttaca 1980
tactttaagg ttattactga ttaatgagaa ttaaagggaag ctgagaatat ataaaaaaaa 2040
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<210> 64

<211> 81

<212> PRT

<213> Homo sapiens

<400> 64

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Met Lys Val Pro Thr Ser His His Ser Asp Glu Lys His Gln Glu Ala
  1              5              10              15

Ser Cys Thr Phe Leu Arg Gly His Ser Arg Ile Asn Pro Pro Leu His
          20              25              30

Thr Ala Ala Ile Ser Ile Met His His Ser Ile Ser Gly Tyr Met His
      35              40              45

Asn Arg Val Phe Leu Gly Ala Ser Leu Gly Phe Ser Ser Ser Ala Ile
      50              55              60

Val Glu Trp Leu His Ser Gln Gly Leu Ala Met Glu Ala His Lys Arg
      65              70              75              80

Ala

```

<210> 65

<211> 581

<212> DNA

<213> Homo sapiens

<400> 65

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ggcatctgtc agctgcctcc tttacagcc atgccttctg gaatctggaa gaggacacca 180
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<210> 66

<211> 67

<212> PRT

<213> Homo sapiens

<400> 66

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Met Cys Val Arg Met Gly Leu Ala His Leu Gly Cys Ser Gly Val Gly
  1             5             10            15
Leu Pro Cys Cys Arg Ala Asp Gly Val Met Leu Trp Ala Gln Gly Ile
          20             25            30
Cys Gln Leu Pro Pro Leu Thr Ala Met Pro Ser Gly Ile Trp Lys Arg
          35             40            45
Thr Pro Leu Leu Gln Ser Leu Gly Ser His Ile Ala Ala Ala Gly Pro
          50             55            60
Arg Arg Ala
  65

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<210> 67

<211> 1916

<212> DNA

<213> Homo sapiens

<400> 67

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acgtttgatg gtggagctgc acaacctcta ccgggccag gtatccccga cggcctcaga 180
catgctgcac atgagatggg acgaggagct ggccgccttc gccaaaggct acgcacggca 240
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<210> 68

<211> 238

<212> PRT

<213> Homo sapiens

<400> 68

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Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu Leu
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Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp Glu Glu
              20              25              30

Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala Gln Val Ser
      35              40              45

Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp Glu Glu Leu Ala
      50              55              60

Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val Trp Gly His Asn Lys
      65              70              75              80

Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe Ala Ile Thr Asp Glu Glu
              85              90              95

Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile Pro Lys Ser Ala
      100             105             110

Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser Arg Ser Pro Glu Asn
      115             120             125

Ser Leu Asp Pro Lys Met Ser Leu Thr Gly Ala Arg Glu Leu Leu Pro
      130             135             140

His Ala Gln Glu Glu Ala Glu Ala Glu Ala Glu Leu Pro Pro Ser Ser
      145             150             155             160

Glu Val Leu Ala Ser Val Phe Pro Ala Gln Asp Lys Pro Gly Glu Leu
              165              170              175

Gln Ala Thr Leu Asp His Thr Gly His Thr Ser Ser Lys Ser Leu Pro
              180              185              190

Asn Phe Pro Asn Thr Ser Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala
      195              200              205

```

Leu Ala Leu Gln Ser Ser Leu Pro Gly Lys Ala His Ser Ile Cys Pro
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Thr Phe Leu Leu Ala Leu Glu Cys Gln Tyr Pro Ala Pro Ala
 225 230 235

<210> 69
 <211> 2051
 <212> DNA
 <213> Homo sapiens

<400> 69
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<210> 70
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 70
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 20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
 225 230 235 240
 Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
 245 250 255
 Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
 260 265 270
 Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
 275 280 285
 Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
 290 295 300
 Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
 305 310 315 320
 Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
 325 330 335
 Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
 340 345 350

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
 355 360 365
 Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
 370 375 380
 Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
 385 390 395 400
 Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
 405 410 415
 Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
 420 425 430

<210> 71

<211> 2557

<212> DNA

<213> Homo sapiens

<400> 71

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<210> 72

<211> 474

<212> PRT

<213> Homo sapiens

<400> 72

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Met Phe Ser Pro Ala Val Ser Lys Ser Cys Phe Ser Pro Trp Val Gly
  1             5             10             15

```

```

Gln Val Thr Glu Asp Cys Ser Ser Lys Trp Ser Lys Tyr Lys His Asp
          20             25             30

```

```

Leu Ala Ala Ser Cys Gln Gly Arg Val Val Ala Ala Glu Glu Lys Asn
      35             40             45

```

```

Gly Val Val Phe Ile Arg Gly Glu Gly Val Gly Ala Tyr Asn Pro Gln
      50             55             60

```

```

Leu Asn Leu Lys Asn Val Gln Arg Asn Leu Ile Leu Leu His Pro Gln
      65             70             75             80

```

```

Leu Leu Leu Leu Val Asp Gln Ile His Leu Gly Glu Glu Ser Pro Leu
          85             90             95

```

```

Glu Thr Ala Ala Ser Phe Phe His Asn Val Asp Val Pro Phe Glu Glu
      100             105             110

```

```

Thr Val Val Asp Gly Val His Gly Ala Phe Ile Arg Gln Arg Asp Gly
      115             120             125

```

```

Leu Tyr Lys Met Tyr Trp Met Asp Asp Thr Gly Tyr Ser Glu Lys Ala
      130             135             140

```

```

Thr Phe Ala Ser Val Thr Tyr Pro Arg Gly Tyr Pro Tyr Asn Gly Thr
      145             150             155             160

```

```

Asn Tyr Val Asn Val Thr Met His Leu Arg Ser Pro Ile Thr Arg Ala
          165             170             175

```

```

Ala Tyr Leu Phe Ile Gly Pro Ser Ile Asp Val Gln Ser Phe Thr Val
      180             185             190

```

```

His Gly Asp Ser Gln Gln Leu Asp Val Phe Ile Ala Thr Ser Lys His
      195             200             205

```

```

Ala Tyr Ala Thr Tyr Leu Trp Thr Gly Glu Ala Thr Gly Gln Ser Ala
      210             215             220

```

```

Phe Ala Gln Val Ile Ala Asp Arg His Lys Ile Leu Phe Asp Arg Asn
      225             230             235             240

```

```

Ser Ala Ile Lys Ser Ser Ile Val Pro Glu Val Lys Asp Tyr Ala Ala
          245             250             255

```


Ile Val Glu Gln Asn Leu Gln His Phe Lys Pro Val Phe Gln Leu Leu
 260 265 270
 Glu Lys Gln Ile Leu Ser Arg Val Arg Asn Thr Ala Ser Phe Arg Lys
 275 280 285
 Thr Ala Glu Arg Leu Leu Arg Phe Ser Asp Lys Arg Gln Thr Glu Glu
 290 295 300
 Ala Ile Asp Arg Ile Phe Ala Ile Ser Gln Gln Gln Gln Gln Ser
 305 310 315 320
 Lys Ser Lys Lys Asn Arg Arg Ala Gly Lys Arg Tyr Lys Phe Val Asp
 325 330 335
 Ala Val Pro Asp Ile Phe Ala Gln Ile Glu Val Asn Glu Lys Lys Ile
 340 345 350
 Arg Gln Lys Ala Gln Ile Leu Ala Gln Lys Glu Leu Pro Ile Asp Glu
 355 360 365
 Asp Glu Glu Met Lys Asp Leu Leu Asp Phe Ala Asp Val Thr Tyr Glu
 370 375 380
 Lys His Lys Asn Gly Gly Leu Ile Lys Gly Arg Phe Gly Gln Ala Arg
 385 390 395 400
 Met Val Thr Thr Thr His Ser Arg Ala Pro Ser Leu Ser Ala Ser Tyr
 405 410 415
 Thr Arg Leu Phe Leu Ile Leu Asn Ile Ala Ile Phe Phe Val Met Leu
 420 425 430
 Ala Met Gln Leu Thr Tyr Phe Gln Arg Ala Gln Ser Leu His Gly Gln
 435 440 445
 Arg Cys Leu Tyr Ala Val Leu Leu Ile Asp Ser Cys Ile Leu Leu Trp
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 Leu Tyr Ser Ser Cys Ser Gln Ser Gln Cys
 465 470

<210> 73

<211> 3442

<212> DNA

<213> Homo sapiens

<400> 73

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```

<210> 74

<211> 61

<212> PRT

<213> Homo sapiens

<400> 74

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Met Lys Lys His Arg Arg Ala Leu Ala Leu Val Ser Cys Leu Phe Leu
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```

```

Cys Ser Leu Val Trp Leu Pro Ser Trp Arg Val Cys Cys Lys Glu Ser
                20                25                30

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Ser Ser Ala Ser Ala Ser Ser Tyr Tyr Ser Gln Asp Asp Asn Cys Ala
 35 40 45

Leu Glu Asn Glu Asp Val Gln Phe Gln Lys Lys Val Pro
 50 55 60

<210> 75

<211> 1159

<212> DNA

<213> Homo sapiens

<400> 75

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<210> 76

<211> 242

<212> PRT

<213> Homo sapiens

<400> 76

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  20 25 30
Gly Ser Gly Gly Ser Gly Val Gly Ile Gly Asp Arg Phe Lys Ile Glu
  35 40 45
Gly Arg Ala Val Val Pro Gly Val Lys Pro Gln Asp Trp Ile Ser Ala
  50 55 60
Ala Arg Val Leu Val Asp Gly Glu Glu His Val Gly Phe Leu Lys Thr
  65 70 75 80
Asp Gly Ser Phe Val Val His Asp Ile Pro Ser Gly Ser Tyr Val Val
  85 90 95
Glu Val Val Ser Pro Ala Tyr Arg Phe Asp Pro Val Arg Val Asp Ile

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100 105 110
 Thr Ser Lys Gly Lys Met Arg Ala Arg Tyr Val Asn Tyr Ile Lys Thr
 115 120 125
 Ser Glu Val Val Arg Leu Pro Tyr Pro Leu Gln Met Lys Ser Ser Gly
 130 135 140
 Pro Pro Ser Tyr Phe Ile Lys Arg Glu Ser Trp Gly Trp Thr Asp Phe
 145 150 155 160
 Leu Met Asn Pro Met Val Met Met Met Val Leu Pro Leu Leu Ile Phe
 165 170 175
 Val Leu Leu Pro Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg
 180 185 190
 Glu Met Glu Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro
 195 200 205
 Asp Val Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly
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 225 230 235 240
 Arg Arg

<210> 77
 <211> 2462
 <212> DNA
 <213> Homo sapiens

<400> 77
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 caagaagtgc ggtggtagct ccaaaaacct cggtggaaag tcatcaggca gacgccaagg 180
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<210> 78

<211> 94

<212> PRT

<213> Homo sapiens

<400> 78

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 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 35 40 45
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 50 55 60
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 65 70 75 80
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly
 85 90

<210> 79

<211> 1178

<212> DNA

<213> Homo sapiens

<400> 79

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 gtcatttctt atgggtgttt catgacgact ttggaagacg tattttttaa gctagaagtt 180
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 gttggatgtc tttgagggat aaaaaaaggc taccatggcc ggagccatag tgaagctatt 600

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ggagaccctg tttaaaaaaa aaaaaaaaaa aaaaaaaa 1178

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<210> 80

<211> 62

<212> PRT

<213> Homo sapiens

<400> 80

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  1             5             10             15

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Ser Ala Leu Asp Ser His Ser Asn Leu Gly Val Ile Ser Tyr Gly Val
      20             25             30

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Ser Met Thr Thr Leu Glu Asp Val Phe Leu Lys Leu Glu Val Glu Ala
      35             40             45

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Glu Ile Asp Gln Ala Gly Lys Asn Arg Thr Asn Lys Thr Phe
      50             55             60

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<210> 81

<211> 1285

<212> DNA

<213> Homo sapiens

<400> 81

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ctgtgtgttc tggaatactc acgtgagggg acttactttg gccagcattg accttcaaag 240
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cattgctttc attttcatag ccacagtgat agccctaaga aaacaactct gtcaaaagct 360
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<210> 82

<211> 61
 <212> PRT
 <213> Homo sapiens

<400> 82
 Met Glu Pro Arg Thr His Pro Thr Trp Leu Leu His Ile Phe Ile Pro
 1 5 10 15
 Ser Cys Ile Ile Ala Phe Ile Phe Ile Ala Thr Val Ile Ala Leu Arg
 20 25 30
 Lys Gln Leu Cys Gln Lys Leu Tyr Ser Ser Lys Asp Thr Thr Lys Arg
 35 40 45
 Pro Val Thr Thr Thr Lys Arg Glu Val Asn Ser Ala Ile
 50 55 60

<210> 83
 <211> 654
 <212> DNA
 <213> Homo sapiens

<400> 83
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 gaaagttcta atctcttccc tctctctgtt gctgccacta atgctgatgt ccatggctc 180
 tagcagcctg aatccagggg tcgccagagg ccacagggac cgaggccagg cttctaggag 240
 atggctccag gaaggcgcc aagaatgtga gtgcaaagat tggttctga gagccccgag 300
 aagaaaattc atgacagtgt ctgggctgcc aaagaagcag tgcccctgtg atcatttcaa 360
 gggcaatgtg aagaaaacaa gacaccaaag gcaccacaga aagccaaaca agcattccag 420
 agcctgccag caatttctca aacaatgtca gctaagaagc tttgctctgc cttttagga 480
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<210> 84
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 84
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 Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His
 20 25 30
 Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln
 35 40 45
 Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe
 50 55 60
 Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys Pro Cys Asp His Phe
 65 70 75 80
 Lys Gly Asn Val Lys Lys Thr Arg His Gln Arg His His Arg Lys Pro
 85 90 95

Asn Lys His Ser Arg Ala Cys Gln Gln Phe Leu Lys Gln Cys Gln Leu
 100 105 110

Arg Ser Phe Ala Leu Pro Leu
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<210> 85
 <211> 1176
 <212> DNA
 <213> Homo sapiens

<400> 85
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<210> 86
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 86
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 20 25 30
 Asp Met Val Phe Gln Ser Val Cys Val Thr Tyr Leu Leu Phe Ile Ser
 35 40 45
 His Cys Arg Trp Leu Cys Leu Leu His His His Lys Lys Phe Lys Leu
 50 55 60
 Cys Ala Leu Ile Asn Cys Val Leu Leu Lys Arg Leu Val Gly
 65 70 75

<210> 87
 <211> 1476
 <212> DNA
 <213> Homo sapiens

<400> 87

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<210> 88

<211> 145

<212> PRT

<213> Homo sapiens

<400> 88

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr
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 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
 20 25 30
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
 35 40 45
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
 50 55 60
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
 65 70 75 80
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Leu Ser Glu Gln Gln Phe
 85 90 95
 Pro Ile Pro Leu Pro Tyr Cys Trp Pro Leu Gln Gly Ser Asp Gln Ala
 100 105 110
 Asp Pro Ser His Asp Ser Gln Gly Cys Ala Ser Cys Gly Ser Gly Pro
 115 120 125
 Gly Val Pro Arg Gly Thr Ser Gly Gly Gly Arg His Leu Pro Val Pro
 130 135 140

Gly
145

<210> 89

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 89

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<210> 90

<211> 61

<212> PRT

<213> Homo sapiens

<400> 90

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  1                      5                      10                      15

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Phe Phe Phe Ser Phe Pro Leu Ser Phe Phe Asn Lys Cys Leu Leu Ile

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20 25 30

Glu Lys Leu Ser Lys Arg Gln Gln Phe Arg Met Asp Ile Leu Thr Asn
35 40 45

Arg His Glu Cys Asn Ser Asp Asn Leu Ile Cys Leu Phe
50 55 60

<210> 91
<211> 1041
<212> DNA
<213> Homo sapiens

<400> 91
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<210> 92
<211> 228
<212> PRT
<213> Homo sapiens

<400> 92
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20 25 30
Pro Ala Val Met Val Leu Leu Leu Ile Glu Thr Ser Ile Ser Val Leu
35 40 45
Leu Val Ala Cys Asn Ile Leu Cys Leu Leu Val Asp Glu Thr Ala Met
50 55 60
Pro Lys Gly Thr Arg Gly Pro Gly Ile Gly Asn Ala Ser Leu Ser Thr
65 70 75 80
Phe Gly Phe Val Gly Ala Ala Leu Glu Ile Ile Leu Ile Phe Tyr Leu
85 90 95
Met Val Ser Ser Val Val Gly Phe Tyr Ser Leu Arg Phe Phe Gly Asn
100 105 110

Phe Thr Pro Lys Lys Asp Asp Thr Thr Met Thr Lys Ile Ile Gly Asn
 115 120 125
 Cys Val Ser Ile Leu Val Leu Ser Ser Ala Leu Pro Val Met Ser Arg
 130 135 140
 Thr Leu Gly Ile Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe
 145 150 155 160
 Asn Trp Leu Gly Asn Phe Tyr Ile Val Leu Ser Tyr Asn Leu Leu Phe
 165 170 175
 Ala Ile Val Thr Thr Leu Cys Leu Val Arg Lys Phe Thr Ser Ala Val
 180 185 190
 Arg Glu Glu Leu Phe Lys Ala Leu Gly Leu His Lys Leu His Leu Pro
 195 200 205
 Asn Thr Ser Arg Asp Ser Glu Thr Ala Lys Pro Ser Val Asn Gly His
 210 215 220
 Gln Lys Ala Leu
 225

<210> 93
 <211> 1792
 <212> DNA
 <213> Homo sapiens

<400> 93
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<210> 94

<211> 254

<212> PRT

<213> Homo sapiens

<400> 94

Met Gly Arg Asp Leu Arg Pro Gly Ser Arg Val Leu Leu Leu Leu Leu
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 20 25 30

Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser Ser Asp Ser
 35 40 45

Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His Leu Arg Ala
 50 55 60

Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu Ser Trp Ser
 65 70 75 80

Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu Met Ser Cys
 85 90 95

Leu Asp Leu Lys Glu Cys Gly His Ala Tyr Ser Gly Ile Val Ala His
 100 105 110

Gln Lys His Leu Leu Pro Thr Ser Pro Pro Thr Ser Gln Ala Ser Glu
 115 120 125

Gly Ala Ser Ser Asp Ile His Thr Pro Ala Gln Met Leu Leu Ser Thr
 130 135 140

Leu Gln Ser Thr Gln Arg Pro Thr Leu Pro Val Gly Ser Leu Ser Ser
 145 150 155 160

Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His Thr Ala Gly
 165 170 175

His Ser Leu Ala Val Gly Pro Glu Ala Gly Glu Asn Gln Lys Gln Pro
 180 185 190

Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr Val Pro Val
 195 200 205

Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala Leu Ser Tyr
 210 215 220

Val Leu Cys Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser Ser Pro Asp
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Leu Pro Val His Tyr Ile Pro Val Ala Pro Asp Ser Asn Thr
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<210> 95

<211> 1234

<212> DNA

<213> Homo sapiens

<400> 95

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<210> 96

<211> 229

<212> PRT

<213> Homo sapiens

<400> 96

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Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
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Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
      20            25            30

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 35             40            45

Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 50             55            60

Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 65             70            75            80

Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
      85            90            95

Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
    100           105           110

Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
    115           120           125

Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
    130           135           140

Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile

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| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|--|--|--|--|--|--|--|--|-----|
| 145 | | | | | | | | | 150 | | | | | | | | | 155 | | | | | | | | | 160 |
| Asn | Ser | Ile | Lys | Ser | Arg | Leu | Ser | Lys | Ser | Gly | His | Ile | Gln | Ile | Leu | | | | | | | | | | | | |
| | | | | 165 | | | | | 170 | | | | | | | | 175 | | | | | | | | | | |
| Leu | Arg | Ala | Phe | Glu | Ala | Arg | Asp | Arg | Asn | Ile | Gln | Glu | Ser | Asn | Phe | | | | | | | | | | | | |
| | | | | 180 | | | | | 185 | | | | | | | | 190 | | | | | | | | | | |
| Asp | Arg | Val | Asn | Phe | Trp | Ser | Met | Val | Asn | Leu | Val | Val | Met | Val | Val | | | | | | | | | | | | |
| | | | | 195 | | | | | 200 | | | | | | | | 205 | | | | | | | | | | |
| Val | Ser | Ala | Ile | Gln | Val | Tyr | Met | Leu | Lys | Ser | Leu | Phe | Glu | Asp | Lys | | | | | | | | | | | | |
| | | | | 210 | | | | | 215 | | | | | | | | 220 | | | | | | | | | | |
| Arg | Lys | Ser | Arg | Thr | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | 225 | | | | | | | | | | | | | | | | | | | | | | | |

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<210> 97
<211> 1204
<212> DNA
<213> Homo sapiens
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| <400> 97 | | | | | | |
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| ttccgggacc | tcgatactga | caggctcatc | agcctgtgcc | tgacccttct | cagcgtgacc | 120 |
| ccagacatcc | tgcaacctga | ggggacattc | ctttgtaaaa | cttggctctg | aagctcaaac | 180 |
| cgtcggttac | agaggagact | gacagaggaa | ttccagaatg | taaggatcat | caaacctgaa | 240 |
| gccagcagga | aagagtcatc | agaaggtgac | ttcttggcca | cacagtacca | cggaaggaag | 300 |
| ggcactgtga | agcagtgagg | atttcttctg | ccattttcat | aatggtcatt | agctcctttt | 360 |
| aagctagaaa | cgtagcctga | gctcctgaag | agttcctggg | agatttctgagc | tgattttgga | 420 |
| gatggagcag | gacaagtgtg | gagtcctctc | ctctctttct | ctctctctct | tttttaacca | 480 |
| aaagagatga | caaaactaag | ttcaggggcc | atggaaaatg | aaaaagctcg | ctatatcttg | 540 |
| atttgggaag | agaaagttat | caagagaag | agtgaggatg | ggaaggatgg | agaaaaacag | 600 |
| actgtgggaa | ggatcagaag | gaatccgccg | aggcagggat | gggtgtgcc | atgtgtgect | 660 |
| tgacgggact | tcattctata | gactgttaaa | ctgtcacaca | caaacaggct | ttccaccctt | 720 |
| gctctgagag | caccacgcac | agatttccag | ttcttagtgt | ggctgtttaa | agtagaaaa | 780 |
| ctgggggctg | ggtagggcca | ctcatgcctg | taaacccagg | gctttagaag | gctcgacctg | 840 |
| ggggattgct | tgaagtccag | agttccaagc | caacctgggc | aacatagcaa | caccgcccat | 900 |
| gtctacaaaa | atgaaaaacc | aaaaagcaaa | caaaaagaaa | aatctgaaat | ttccatctgg | 960 |
| ggattaactt | ctgtctttct | ggtgaacaat | atagcaattc | acgcattctt | caagcagcaa | 1020 |
| aagttcccgg | aacaattagg | gaagacgtat | ggtctgaatt | tatcaggcca | gtgggtctgc | 1080 |
| cttgggtttt | gctggaaatt | tatatcagtg | tctgggctcc | caagaacata | aatgtaattg | 1140 |
| ccaaagcaaa | aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | 1200 |
| aaaa | | | | | | 1200 |

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<210> 98
<211> 92
<212> PRT
<213> Homo sapiens
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<400> 98
Met Ala Pro Asn Ala Thr Gly Phe Arg Asp Leu Asp His Asp Arg Leu
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Ile Ser Leu Cys Leu Thr Leu Leu Ser Val Thr Pro Asp Ile Leu Gln
      20             25             30

Pro Gly Gly Thr Phe Leu Cys Lys Thr Trp Ala Gly Ser Gln Ser Arg
    35             40             45

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Arg Leu Gln Arg Arg Leu Thr Glu Glu Phe Gln Asn Val Arg Ile Ile
50 55 60

Lys Pro Glu Ala Ser Arg Lys Glu Ser Ser Glu Val Tyr Phe Leu Ala
65 70 75 80

Thr Gln Tyr His Gly Arg Lys Gly Thr Val Lys Gln
85 90

<210> 99

<211> 1343

<212> DNA

<213> Homo sapiens

<400> 99

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<210> 100

<211> 210

<212> PRT

<213> Homo sapiens

<400> 100

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Pro Ala Leu Gly Ser Arg Ile Ala Gly Ile Thr Gly Lys His His His
20 25 30

Leu Trp Leu Ile Phe Ile Phe Leu Val Glu Thr Gly Phe His His Val
35 40 45

Gly His Ala Ser Ile Ser Ser Phe Leu Ile Thr Asp Lys Ser Arg Pro
50 55 60

Lys Ile Ser Gly Thr Arg Tyr His Gln Val Arg Leu Pro Thr Phe Val

| | | | | | | | |
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| ctcagccccc | ggcttccccc | atctgcccac | agccaacccc | acagggcctg | gggagcgggg | 120 | |
| cccgccgggg | gcagtggagg | tgatccggga | gtccagcagc | accacgggca | tggttggtgg | 180 | |
| catctgtygc | gcggcggcgc | tctgcattct | caticctctc | tacggcatgt | ataagtaccg | 240 | |
| caatcgtgat | gagggctcct | accaggtgga | ccagagccga | aactacatca | gtaactcggc | 300 | |
| ccagagcaat | ggggcggttg | tgaaagagaa | ggccccggct | gcccccaaga | cgcccagcaa | 360 | |
| ggccaagaag | aacaaagaca | aggagtatta | tgtctgagcc | cccggcactg | cgccccactg | 420 | |
| ccagctgccc | ctcctgggag | ggccccggag | gagggtgcc | ccctctccct | gccaggggcc | 480 | |
| tggggacctt | ctccctgggt | gcctcaggct | tctcttacga | agaggaaacg | caaaaaaaga | 540 | |
| aaagaaaaaa | ccccgtgctc | gcccccttec | tctgcgcgtc | cactgcgcgg | cctcgtcagt | 600 | |
| ccccgggctg | actgtccctc | tcagctctgc | gcctgcacag | cagggcacgt | gctcacagcc | 660 | |
| ctgggttgat | ttattttttt | aagggggtag | ttttattttg | gtggggttgg | gtgggaagga | 720 | |
| aggctggggg | ttttgtaaag | tgtccactgc | tcgtcctggt | aattttcctc | aatttttctt | 780 | |
| cttcttcctt | ctgtccctcc | tgcccttcctt | ctcttcccaa | gccttccaat | ccccatccca | 840 | |
| ggcttctgtg | gtctcactgt | ccccaccctc | cttccctact | tctttttttg | tgtgtctggt | 900 | |
| tctctccctc | ctttctcccc | tttgggtttc | cagagtccgt | gggagaaggg | cgggagggtg | 960 | |
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| ttccacgagc | agcagctgtg | ggcacccgct | gggcgcgggc | agcagggga | agggagcaag | 1260 | |
| gcatttgtcca | cagactcgtg | gggtcacttc | tttggccagc | ggctccctgc | tcceccagtt | 1320 | |
| ttttttctct | ctttgttaac | aaatgtgtct | gagtcttgga | aaacacccca | accccgaaa | 1380 | |
| tgtgtgggaa | aaagaaaaaca | aaaactttcc | aaattccaaa | aaaaaaaaaa | aaaaaaaaaa | 1440 | |

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 <213> Homo sapiens

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 Ala Val Val Lys Glu Lys Ala Pro Ala Ala Pro Lys Thr Pro Ser Lys
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 Ala Lys Lys Asn Lys Asp Lys Glu Tyr Tyr Val
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<210> 103
 <211> 733
 <212> DNA
 <213> Homo sapiens

<400> 103
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 <212> PRT
 <213> Homo sapiens

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 Trp Lys Gly Asn Lys Asn Thr Asp Tyr Ser Glu Gln Phe Ser Pro Lys
 35 40 45

Arg Ile Ala Phe

50

<210> 105

<211> 2342

<212> DNA

<213> Homo sapiens

<400> 105

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<210> 106

<211> 431

<212> PRT

<213> Homo sapiens

<400> 106

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 20 25 30
 Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu Ser Lys Gly
 35 40 45
 Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln Glu Asp Cys Ile
 50 55 60
 Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly Asp Lys Ala Cys Asn
 65 70 75 80
 Leu Met Ile Phe Asp Thr Arg Lys Thr Ala Arg Gln Pro Asn Cys Tyr
 85 90 95
 Leu Phe Phe Cys Pro Asn Glu Glu Ala Cys Pro Leu Lys Pro Ala Lys
 100 105 110
 Gly Leu Met Ser Tyr Arg Ile Ile Thr Asp Phe Pro Ser Leu Thr Arg
 115 120 125
 Asn Leu Pro Ser Gln Glu Leu Pro Gln Glu Asp Ser Leu Leu His Gly
 130 135 140
 Gln Phe Ser Gln Ala Val Thr Pro Leu Ala His His His Thr Asp Tyr
 145 150 155 160
 Ser Lys Pro Thr Asp Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe
 165 170 175
 Gly Ser Ser Asp His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser
 180 185 190
 Ala Gln Leu Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln
 195 200 205
 Phe Ser Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser
 210 215 220
 Ala Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
 225 230 235 240
 Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr Pro
 245 250 255
 Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro Val Thr
 260 265 270
 Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr Val Phe Thr
 275 280 285
 Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr Ala Val Leu Thr
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 Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly Ser Leu Glu Thr Ile
 305 310 315 320
 Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu Asn Thr Gly Asn Val Tyr
 325 330 335

Asn Pro Thr Ala Leu Ser Met Ser Asn Val Glu Ser Ser Thr Met Asn
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 Lys Thr Ala Ser Trp Glu Gly Arg Glu Ala Ser Pro Gly Ser Ser Ser
 355 360 365
 Gln Gly Ser Val Pro Glu Asn Gln Tyr Gly Leu Pro Phe Glu Lys Trp
 370 375 380
 Leu Leu Ile Gly Ser Leu Leu Phe Gly Val Leu Phe Leu Val Ile Gly
 385 390 395 400
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<210> 107

<211> 3153

<212> DNA

<213> Homo sapiens

<400> 107

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<210> 108

<211> 102

<212> PRT

<213> Homo sapiens

<400> 108

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Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
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Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
          20              25              30

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```

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
      35              40              45

```

```

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
      50              55              60

```

```

Pro Glu Asn Lys Ala Ser Glu Leu Ser Phe Pro Met Ser Ser Leu Ile
      65              70              75              80

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Gln Met Glu Ala Val Lys Val Lys Thr Leu Lys Ser Leu Thr Glu Pro
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Pro Ala Met Gly Leu Cys
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<210> 109

<211> 1805

<212> DNA

<213> Homo sapiens

<400> 109

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<210> 110

<211> 406

<212> PRT

<213> Homo sapiens

<400> 110

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Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
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Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
          20              25              30

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
          35              40              45

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
          50              55              60

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
          65              70              75              80

Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
          85              90              95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys
          100             105             110

Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys
          115             120             125

Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser
          130             135             140

Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys
          145             150             155             160

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Asp Pro Leu Gly Gln Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln
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 Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala
 180 185 190
 Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val
 195 200 205
 Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg
 210 215 220
 Pro Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
 225 230 235 240
 Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val
 245 250 255
 Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr
 260 265 270
 Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala
 275 280 285
 Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln
 290 295 300
 Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn
 305 310 315 320
 Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn
 325 330 335
 Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser
 340 345 350
 Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg
 355 360 365
 Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu
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 Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg
 385 390 395 400
 Lys Lys Glu Glu Glu Val
 405

<210> 111

<211> 2824

<212> DNA

<213> Homo sapiens

<400> 111

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<210> 112

<211> 399

<212> PRT

<213> Homo sapiens

<400> 112

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Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser Ser Glu Gln Asp Gly
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Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln Arg Leu Lys Thr Lys
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Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile Ile Ser Arg Tyr
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 Ala Phe Thr Thr Val Ser Cys Arg Met Leu Asn Arg Ala Ser Glu Asp
 65 70 75 80
 Gln Asp Ile Glu Phe Gln Met Gln Ile Pro Ala Ala Ala Phe Ile Thr
 85 90 95
 Asn Phe Thr Met Leu Ile Gly Asp Lys Val Tyr Gln Gly Glu Ile Thr
 100 105 110
 Glu Arg Glu Lys Lys Ser Gly Asp Arg Val Lys Glu Lys Arg Asn Lys
 115 120 125
 Thr Thr Glu Glu Asn Gly Glu Lys Gly Thr Glu Ile Phe Arg Ala Ser
 130 135 140
 Ala Val Ile Pro Ser Lys Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu
 145 150 155 160
 Glu Leu Leu Gln Arg Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val
 165 170 175
 Arg Pro Gln Gln Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu
 180 185 190
 Glu Ser Ala Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser
 195 200 205
 Arg Gln Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro
 210 215 220
 Ser Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys
 225 230 235 240
 Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu Gly
 245 250 255
 Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile Gly Asp
 260 265 270
 Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala Pro Lys Asp
 275 280 285
 Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu Asp Ser Ser Ala
 290 295 300
 Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys Asp Ala Leu Phe Thr
 305 310 315 320
 Ile Leu His Asp Leu Arg Pro Gln Asp Arg Phe Ser Ile Ile Gly Phe
 325 330 335
 Ser Asn Arg Ile Lys Val Trp Lys Asp His Leu Ile Ser Val Thr Pro
 340 345 350
 Asp Ser Ile Arg Asp Gly Lys Val Tyr Ile His His Met Ser Pro Thr
 355 360 365

Gly Gly Lys Asp Asp Thr Phe Phe Ser His Trp Leu Gly Phe Glu Ile
 370 375 380

Met Phe Ser Phe Phe Val Phe Phe Phe Cys Phe Phe Ala Lys Arg
 385 390 395

<210> 113
 <211> 1711
 <212> DNA
 <213> Homo sapiens

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 gtataacctg ctttctttt tacatttatt aaaagtggat tttgtaaaag catttcattg 180
 acacgcgacc tatcacagac aatggaattc gtcagtgggt gtaagactga aatcctgatg 240
 cttttcacac ttcttgctc ttgctatgta tttctgcctc tagccttgcc atgttttgcc 300
 tttttttttc tttttggcca attccttttt atatgtgccc acaacagagg tggggagaca 360
 cggagcacc tgggtcctc ccagcgctgc tgggcaggcc ccgtctccag gccccagctg 420
 ttgaaacttt gaagggcaac aaacaacat ccacactgcc ggaccctagg ctgttcaggg 480
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<210> 114
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 114
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 20 25 30

Ala Phe Phe Phe Leu Phe Gly Gln Phe Leu Phe Ile Cys Ala His Asn
 35 40 45

Arg Gly Gly Glu Thr Arg Ser Thr Leu Gly Pro Ser Gln Arg Cys Trp
 50 55 60

Ala Gly Pro Val Ser Arg Pro Gln Leu Leu Lys Leu
 65 70 75

<210> 115
 <211> 2116
 <212> DNA
 <213> Homo sapiens

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<210> 116
 <211> 359
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe Gln Val Lys Ala
 50 55 60
 Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val Ser Tyr Asp Trp Leu
 65 70 75 80
 Ile Leu Gln Gly Pro Ala Lys Pro Val Phe Glu Gly Asp Leu Leu Val
 85 90 95
 Leu Arg Cys Gln Ala Trp Gln Asp Trp Pro Leu Thr Gln Val Thr Phe
 100 105 110
 Tyr Arg Asp Gly Ser Ala Leu Gly Pro Pro Gly Pro Asn Arg Glu Phe
 115 120 125
 Ser Ile Thr Val Val Gln Lys Ala Asp Ser Gly His Tyr His Cys Ser
 130 135 140
 Gly Ile Phe Gln Ser Pro Gly Pro Gly Ile Pro Glu Thr Ala Ser Val
 145 150 155 160
 Val Ala Ile Thr Val Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala
 165 170 175
 Val Pro Ser Ala Glu Pro Gln Ala Gly Gly Pro Met Thr Leu Ser Cys
 180 185 190
 Gln Thr Lys Leu Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser
 195 200 205
 Phe Tyr Lys Asp Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu
 210 215 220
 Phe Gln Ile Pro Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys
 225 230 235 240
 Glu Ala Ala Thr Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln Leu
 245 250 255
 Glu Ile Arg Val Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro Thr Leu
 260 265 270
 Asn Pro Ala Pro Gln Lys Ser Ala Ala Pro Gly Thr Ala Pro Glu Glu
 275 280 285
 Ala Pro Gly Pro Leu Pro Pro Pro Pro Thr Pro Ser Ser Glu Asp Pro
 290 295 300
 Gly Phe Ser Ser Pro Leu Gly Met Pro Asp Pro His Leu Tyr His Gln
 305 310 315 320
 Met Gly Leu Leu Leu Lys His Met Gln Asp Val Arg Val Leu Leu Gly
 325 330 335
 His Leu Leu Met Glu Leu Arg Glu Leu Ser Gly His Arg Lys Pro Gly
 340 345 350

Thr Thr Lys Ala Thr Ala Glu
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<211> 1391
<212> DNA
<213> Homo sapiens

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aaaaaaaaa a 1391

<210> 118
<211> 56
<212> PRT
<213> Homo sapiens

<400> 118
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20 25 30
Lys Pro Ser Pro His His Met Ala Ser Asp Arg Phe Leu Pro Ser Arg
35 40 45
Lys Phe Cys Gly Cys Ala Val Leu
50 55

<210> 119
<211> 21
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<220>

<223> oligonucleotide

<400> 119
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<210> 120
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 120
acgctcaact ccacctcc 18

<210> 121
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<220>
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<400> 121
cttgggaacat agcaccactc c 21

<210> 122
<211> 20
<212> DNA
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<220>
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<400> 122
ccattccaga cttccctgtc 20

<210> 123
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<400> 123
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<400> 125
gaacagatgg actctcccc

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<210> 126
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21

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<400> 128
ccgatcaatt ttacacaaca a

21

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<210> 130
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<400> 130
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<210> 131
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<400> 131
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<210> 133
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<210> 135
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<400> 137
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<210> 138
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<210> 139
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<210> 141
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<210> 144
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<210> 146
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aacaggcact ttgaagtcag c 21

<210> 147
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<400> 147
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<210> 148
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<212> DNA
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<210> 149
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<210> 151
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<400> 151
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<210> 152
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<213> Artificial Sequence

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20

<210> 153

<211> 20

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20

<210> 154

<211> 21

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<213> Artificial Sequence

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<400> 154

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21

<210> 155

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide

<400> 155

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21

<210> 156

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide

<400> 156

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<210> 157

<211> 20

<212> DNA

<213> Artificial Sequence

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<400> 158
tcattcaaca accagaacgt g 21

<210> 159
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<220>
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<400> 160
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<210> 161
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<220>
<223> oligonucleotide

<400> 161
tacctcacgc ctgtaatccc 20

<210> 162
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 162
gaggagctat ggacgtctgc 20

<210> 163
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 163
agttcattca gccttatata a

21

<210> 164
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 164
ctagggttctg aagaggggcc

20

<210> 165
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 165
ctgaggccag ttgtttccat

20

<210> 166
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 166
ggatcagcag gattacttgc a

21

<210> 167
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 167
ttcacgcatt cttcaagcag

20

<210> 168
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 168
cctgaaatct ttggccttga

20

<210> 169
<211> 113
<212> PRT
<213> Homo sapiens

<400> 169
Met Val Leu Thr Leu Trp Cys Asn Leu Cys Ser Arg Ala Ser Ser Trp
1 5 10 15
Val Arg Gln Lys His Val Ser Cys Cys Val His Asn Tyr Thr Gln Pro
20 25 30
Phe Leu Leu Ile Gln Ser Ser Phe Trp Ala Met Ser Ser Glu Thr Lys
35 40 45
Pro Lys Ala Leu Ser Lys Asp Tyr Leu Cys Ile Ser Tyr Arg Ser Pro
50 55 60
His Ser Thr Pro Thr His Arg His Ser Ser Asn Ser Ser Tyr Asp Leu
65 70 75 80
Pro Val Glu Ala Gln Ala Ser Tyr Leu Asp Ile Lys Ser Leu His Gly
85 90 95
Gln Ser Gly Leu Cys Leu Ser Arg Phe Ile Phe His Tyr His Thr Pro
100 105 110

Tyr

<210> 170
<211> 321
<212> PRT
<213> Homo sapiens

<400> 170
Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu
1 5 10 15
Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly
20 25 30
Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln
35 40 45
Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu
50 55 60
Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu
65 70 75 80
Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr
85 90 95
Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser

100 105 110
 Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val
 115 120 125
 Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu
 130 135 140
 Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val
 145 150 155 160
 Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys
 165 170 175
 Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu
 180 185 190
 Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His
 195 200 205
 Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe
 210 215 220
 His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp Ile
 225 230 235 240
 Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala Ala
 245 250 255
 Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe Leu
 260 265 270
 Ala Ala Gly Ser Gly Cys Thr Ser Ser Trp Trp Arg Ala Pro Pro Trp
 275 280 285
 Pro Ser Ser Cys Ser Arg Ala Thr Ser Ser Ser Pro Gln Glu Thr Thr
 290 295 300
 Arg Thr Cys Ser Cys Pro Arg Arg Thr Arg Arg Met Phe Arg Trp Ser
 305 310 315 320
 Lys

<210> 171

<211> 39

<212> PRT

<213> Homo sapiens

<400> 171

Met Gln Arg Val Glu Val Phe Ser Thr Gln Glu Leu Ala Asp Val Asn
 1 5 10 15

Glu Val Leu Arg Met Gly Pro Ser Pro Ile Ser Val Ala Ser Thr Glu
 20 25 30

Phe Cys Tyr Pro Ser Phe Arg
 35

<210> 172

<211> 193

<212> PRT

<213> Homo sapiens

<400> 172

Gly Trp Gly His Leu Leu Phe Leu Trp Pro Val Leu Ser Phe Val Ile
 1 5 10 15

Leu Pro Leu Gly Lys Glu Cys Gln Trp Thr Asp Ala Cys Leu Ser His
 20 25 30

Pro Cys Ala Asn Gly Ser Thr Cys Thr Thr Val Ala Asn Gln Phe Ser
 35 40 45

Cys Lys Cys Leu Thr Gly Phe Thr Gly Gln Lys Cys Glu Thr Asp Val
 50 55 60

Asn Glu Cys Asp Ile Pro Gly His Cys Gln His Gly Gly Thr Cys Leu
 65 70 75 80

Asn Leu Pro Gly Ser Tyr Gln Cys Gln Cys Leu Gln Gly Phe Thr Gly
 85 90 95

Gln Tyr Cys Asp Ser Leu Tyr Val Pro Cys Ala Pro Ser Pro Cys Val
 100 105 110

Asn Gly Gly Thr Cys Arg Gln Thr Gly Asp Phe Thr Phe Glu Cys Asn
 115 120 125

Cys Leu Pro Gly Lys Glu Leu Pro Ser Val Pro Gly Leu Gly Asp Lys
 130 135 140

Pro Leu Ala Gln Glu Val Val Gly Val Ala Gln Leu Phe Phe Leu Gly
 145 150 155 160

Ser Ala Arg Lys Lys Gly Ser Glu Asn Phe Val Gly Gly Gly Leu Leu
 165 170 175

Val Arg Glu Glu Phe Tyr Gly Pro Thr Val Val His Lys Leu Ser Arg
 180 185 190

Gly

<210> 173

<211> 72

<212> PRT

<213> Homo sapiens

<400> 173

Met Pro Ala Cys Leu Ile Pro Val Gln Met Glu Val Pro Val Pro Leu
 1 5 10 15

Trp Pro Thr Ser Ser Pro Ala Asn Ala Ser Gln Ala Ser Gln Gly Arg
 20 25 30

Ser Val Arg Leu Met Ser Met Ser Val Thr Phe Gln Asp Leu Pro Ala

35 40 45
 Trp Trp His Leu Pro Gln Pro Ala Trp Phe Leu Pro Val Pro Val Pro
 50 55 60
 Ser Gly Leu His Arg Pro Val Leu
 65 70

<210> 174
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 174
 Met Leu Arg Ala Gly Ala Ala Gln Thr Cys Ser Ala Gly Leu Gln Val
 1 5 10 15
 Leu Lys Pro Tyr Trp Gly Trp Val Gly Ser Gly Ala Ala Ala Phe Ala
 20 25 30
 Thr Leu Arg Ile Gly Ala Lys Ala Thr Asp Val Tyr Leu Thr Val Thr
 35 40 45
 Leu His Trp Val Leu Lys Glu Ile Ile Ser Arg Cys Asn Tyr Asn Tyr
 50 55 60
 Cys Leu Leu Arg Lys Ile Trp Glu Phe
 65 70

<210> 175
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 175
 Met Val Leu Val Ser Ser Phe Phe Val Phe Tyr Ser Val His Ser Phe
 1 5 10 15
 Leu Thr Ile Trp Thr Thr Val Val Ala Asn Pro Gly Gln Trp Ile Val
 20 25 30
 Thr Asn Ser Val Leu Val Ala Ser Cys Phe Pro Ala Arg Ser Pro Phe
 35 40 45
 Val Leu Ile Met Ser Asp Thr His Ile Ser Gln Phe Cys Phe Ala Cys
 50 55 60
 Arg Thr Arg Lys Thr Leu Phe Pro Asn Leu Val Val Met Pro
 65 70 75

<210> 176
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 176
 Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp Phe Ala

1 5 10 15
 Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala Gly
 20 25 30
 Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val Pro
 35 40 45
 Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His
 50 55 60
 Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe
 65 70 75 80
 Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu
 85 90 95
 Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly
 100 105 110
 Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val
 115 120 125
 Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe Tyr
 130 135 140
 Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr Leu Val
 145 150 155 160
 Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro Val Leu
 165 170 175
 Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro Glu Thr
 180 185 190
 Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys Gly
 195 200 205
 Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr Val Arg
 210 215 220
 Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu Glu Glu
 225 230 235 240
 Ala Glu Cys Val Pro Asp Asn Cys Val
 245

<210> 177

<211> 191

<212> PRT

<213> Homo sapiens

<400> 177

Met Ile Thr Val Asp Ile Ile Pro Ser Gly Trp Asn Ser Ala Asp Gly
 1 5 10 15
 Lys Ser Asp Lys Thr Lys Ser Ala Pro Ser Arg Asp Pro Glu Arg Leu
 20 25 30

Gln Lys Ile Lys Glu Ser Leu Leu Leu Glu Asp Ser Glu Glu Glu Glu
 35 40 45
 Gly Asp Leu Cys Arg Ile Cys Gln Met Ala Ala Ala Ser Ser Ser Asn
 50 55 60
 Leu Leu Ile Glu Pro Cys Lys Cys Thr Gly Ser Leu Gln Tyr Val His
 65 70 75 80
 Gln Asp Cys Met Lys Lys Trp Leu Gln Ala Lys Ile Asn Ser Gly Ser
 85 90 95
 Ser Leu Glu Ala Val Thr Thr Cys Glu Leu Cys Lys Glu Lys Leu Glu
 100 105 110
 Leu Asn Leu Glu Asp Phe Asp Ile His Glu Leu His Arg Ala His Ala
 115 120 125
 Asn Glu Gln Ala Glu Tyr Glu Phe Ile Ser Ser Gly Leu Tyr Leu Val
 130 135 140
 Val Leu Leu His Leu Cys Glu Gln Ser Phe Ser Asp Met Met Gly Asn
 145 150 155 160
 Thr Asn Glu Pro Ser Thr Arg Val Arg Leu Gln Arg Met Ile Pro Lys
 165 170 175
 Lys Thr Glu Thr Ile Thr Gly His Leu Ile Leu Pro Asn Phe Ile
 180 185 190

<210> 178

<211> 80

<212> PRT

<213> Homo sapiens

<400> 178

Met Phe Leu Ala Cys Leu Cys Leu Glu Asn Trp Ser Ser Gln Ala Pro
 1 5 10 15
 Leu Ala Ala Thr Ser Pro Cys Trp Ala Ser Glu Thr Ser Leu Cys Leu
 20 25 30
 Val Ser Tyr Tyr Ala Leu Ser Phe Ala Met Thr Thr Thr Lys Ser Lys
 35 40 45
 Pro Val Gly Thr Pro Val Gly Pro Leu Asp Leu Pro Thr Ser Pro Gly
 50 55 60
 Ala Cys Arg Arg Ser Pro Thr Phe Thr Ala Pro Ser Ser Asp Thr Leu
 65 70 75 80

<210> 179

<211> 62

<212> PRT

<213> Homo sapiens

<400> 179

Met Pro Gly Phe Ala Gly Phe Ile Cys Leu Ile Leu Phe Cys Val Phe

1 5 10 15
 Ser Trp Leu Phe Gly Ser Phe Pro Gly Thr Leu Asp Gly Ser Ile Pro
 20 25 30
 Arg His Leu Val Ile Lys Gln Leu Ser Pro Thr Pro Tyr His Gly Lys
 35 40 45
 Arg Gly Arg Asn Ile Ala Pro Ser Leu Ile Thr Tyr His Leu
 50 55 60

<210> 180
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Leu Gly Ser Leu Gly Asp Ala Arg Phe Cys Gly Phe Tyr Leu Phe
 1 5 10 15
 Asn Phe Ile Leu Cys Phe Leu Leu Ala Leu Trp Val Phe Pro Gly Tyr
 20 25 30
 Thr Arg Trp Leu His Pro Lys Ala Ser Cys His Lys Thr Ala Phe Pro
 35 40 45
 His Pro Ile Ser Trp Glu Lys Gly Glu Lys Tyr Ser Pro
 50 55 60

<210> 181
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 181
 Met Met Ile Ser Leu His Thr Val Gln Ser His Asn Leu Lys Ile Lys
 1 5 10 15
 Leu Ser Trp Leu Cys Phe Leu Cys Ser Cys Gln Asn Ile Gly Thr Ile
 20 25 30
 Gly Arg Ser Lys Thr Phe Ile Leu Leu Leu Gln Val Tyr Leu Gly Thr
 35 40 45
 Phe Thr Cys Val Phe Lys Gly Ile Ser Phe Gln Gln
 50 55 60

<210> 182
 <211> 227
 <212> PRT
 <213> Homo sapiens

<400> 182
 Met Met Gly Ser Glu Ala Ala Gly Arg Gly Ser Gln Glu Leu Leu Val
 1 5 10 15
 Val Gln Pro Val Leu Pro Ser Glu Ala Leu Leu Phe Pro Gly Leu Pro

20 25 30
 Ala Gly Phe Ser Arg Arg Leu Ser Ser Asn Ala Gly Pro Arg Leu Leu
 35. 40 45
 Ala Trp Val Leu Ala Cys Pro Leu Arg Pro Leu Ala Ala Cys Leu Leu
 50 55 60
 Ser Leu Val Ala Leu Pro Gly Cys Trp Ala Ala Leu Ser Gly Arg Leu
 65 70 75 80
 Leu Pro Val Cys Phe Pro Trp Trp Leu Cys Leu Gly Ala Gly Pro Ala
 85 90 95
 Phe Ser Gly Cys Leu Leu Pro Val Tyr Cys His Leu Gln Arg Gly Ser
 100 105 110
 Leu Leu Arg Pro Thr Leu Leu His Leu Ala Pro Pro Trp Leu Leu Ala
 115 120 125
 Trp Pro Asn Leu Ala Phe Cys Ala Met Leu Glu Leu Glu Leu Leu Leu
 130 135 140
 Phe Phe Arg Gly Gly Asn Arg Val Glu Ser Gly Lys Gly Leu Ala Pro
 145 150 155 160
 Lys Cys Cys Cys Cys Gly Phe Phe Ala Phe Ser Lys Asp Ala Leu Pro
 165 170 175
 Gly Pro Lys Leu Gln Thr Ala Val Leu Ser Lys Gln Val Arg Ser Leu
 180 185 190
 Gly Phe Gly Ala His Leu Leu Ser Gly Ser Ile Ser Ile Leu Leu Leu
 195 200 205
 Ala Thr Ser Gly Gln Arg Pro Pro Gln Pro His Ile Ala Arg Cys Trp
 210 215 220
 Gln Lys Gly
 225

<210> 183

<211> 97

<212> PRT

<213> Homo sapiens

<400> 183

Met Leu Ser Cys Thr Leu Gly Leu Thr Val Cys Pro Leu Ser Pro Ala
 1 5 10 15
 Pro Ser Val Thr Leu Ala Val Ala Leu Asn Gly Gln Leu Arg Arg Pro
 20 25 30
 Leu Cys Cys Ser Ser Ala Phe Pro Glu Val Gly Glu Pro Ala Trp Pro
 35 40 45
 Arg Pro Leu Ser Ser Asp Gln Ala Leu Ser Pro Arg Ser Tyr Gly Arg
 50 55 60

Pro Gly Ser Gly Val Gly Thr His Gly Pro Gly Trp Gly Gly Ala Gln
65 70 75 80

Ser Asp Val Asn Phe Phe Pro Cys Val Asp Met Tyr Ser Gln Arg Val
85 90 95

Val

<210> 184

<211> 68

<212> PRT

<213> Homo sapiens

<400> 184

Met Cys Phe Leu Leu Phe Gly Ser Leu Cys Ile Tyr Tyr Phe Ser Leu
1 5 10 15

Phe Leu Val Phe Phe Phe Ser Cys Phe Cys Phe Val Trp Cys Phe Val
20 25 30

Pro Val Phe Ile Val Ser Gly Ile Ser Leu Pro Leu Trp Ile Pro His
35 40 45

Gly Leu Asp Arg Asp Gly Pro Val Met Pro Ser Ser Phe Leu Leu Leu
50 55 60

Leu Leu Leu Trp
65

<210> 185

<211> 142

<212> PRT

<213> Homo sapiens

<400> 185

Met Phe Ser Cys Asn Glu Asn Ser Ile Phe Phe Arg Ile Gly Phe Val
1 5 10 15

Phe Ile Leu Leu Ser Phe Ile Ser Ser Cys Gln Thr Leu Asn Gly Tyr
20 25 30

Val Cys Ile Leu Ile Thr Leu Phe Ser Leu Leu Trp Lys Arg Arg Thr
35 40 45

Arg Glu Gln Met Leu Leu Arg Ala Gly Val Ser Glu Lys Asn Leu Ser
50 55 60

Met Leu Phe Asn Val Phe Leu Pro Leu Pro His Ser Val Cys Val Thr
65 70 75 80

Phe Tyr Asn Ile Lys Lys Tyr Tyr Asn Ile Ser Arg Ile Trp Asn Cys
85 90 95

His His Asp Glu Trp Pro Phe Gln Cys Ile Val Thr Glu Ile Pro Glu
100 105 110

Asp Ser Pro Gly Leu Gln Phe His Trp Phe Leu Leu Gln Phe Leu Val

115 120 125

Ala Val Ile Val Ala Val Ser Ser Leu Lys Asp Leu Leu Trp
 130 135 140

<210> 186
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 186
 Met Ser Cys Pro Leu Pro Leu Leu Ile Ser Ala Ile Ala Ala Val Gly
 1 5 10 15
 Ser Ser Met Gln Thr His Ala Arg Ala Ser Phe Ala Ala Gly Pro Ser
 20 25 30
 Gln Glu Asp Phe Ser Ala His Leu Ala Gln Asp Gln His Ser Pro Glu
 35 40 45
 Val Gln Gly His Tyr His Ala Arg Gly Asn Pro Pro Ala Val Gly Asp
 50 55 60
 Thr Ser Leu Trp Met Lys Val Pro Thr Ser His His Ser Asp Glu Lys
 65 70 75 80
 His Gln Glu Ala Ser Cys Thr Phe Leu Lys Arg Pro Gln Gln Asp Gln
 85 90 95
 Ser Pro Ile Ala His Ser Ser His Leu Asn Asn Ala Pro Phe Tyr
 100 105 110

<210> 187
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 187
 Met Phe Gly Met Pro His Thr Met Ser Cys Pro Leu Pro Leu Leu Ile
 1 5 10 15
 Ser Ala Ile Ala Ala Val Gly Ser Ser Met Gln Thr His Ala Arg Ala
 20 25 30
 Ser Phe Ala Ala Gly Pro Ser Gln Lys Thr Ser Gln Pro Ile Trp Ser
 35 40 45
 Arg Ile Phe Leu Pro Leu Lys Val Thr Ala Pro Lys Ser Cys Pro Met
 50 55 60
 Phe Tyr Phe Gln Glu Phe Pro Asn
 65 70

<210> 188
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 188

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
 20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
 35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
 50 55 60

Tyr Leu Glu Thr Gly Met Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Arg Pro
 85 90 95

Gln Gln Arg Arg Gln Arg Pro Pro Arg Cys Gly Arg Pro
 100 105

<210> 189

<211> 76

<212> PRT

<213> Homo sapiens

<400> 189

Met Trp Pro Ala Leu His Leu Leu His His Trp Ala Val Trp Gly Cys
 1 5 10 15

Arg Leu His His His His Asp Pro Pro Pro Gly Leu Cys His Pro Ser
 20 25 30

Phe Leu Pro Ser Leu Trp Pro His Cys His Cys Gly Gly Arg Ala Gly
 35 40 45

Gly Gly Cys Gly Leu Cys Cys Pro Pro Ala Gln Ser Leu Arg Ala Gly
 50 55 60

Pro Ser Lys Ala Thr Gly Lys Glu Gly Cys Ala Cys
 65 70 75

<210> 190

<211> 168

<212> PRT

<213> Homo sapiens

<400> 190

Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys Gly
 1 5 10 15

Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu Val
 20 25 30

Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile Leu
 35 40 45

Leu Asp Thr..Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg Leu
 50 55 60
 Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Glu Trp Leu
 65 70 75 80
 Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser Val Thr Thr Gln Ala
 85 90 95
 Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala Met Leu Gln Ala Cys
 100 105 110
 Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys Gln Phe Val Glu Gln
 115 120 125
 His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg Gly Trp Asp Ala His
 130 135 140
 Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr Met Ser Ser Pro Leu
 145 150 155 160
 Gln Cys Ile His Ser Pro Asp Leu
 165

<210> 191

<211> 272

<212> PRT

<213> Homo sapiens

<400> 191

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
 1 5 10 15
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
 20 25 30
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
 35 40 45
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
 50 55 60
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
 65 70 75 80
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Leu Ser Glu Gln Gln Phe
 85 90 95
 Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg
 100 105 110
 Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln
 115 120 125
 Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu
 130 135 140
 Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met

145 150 155 160
 Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met Asp Asp
 165 170 175
 Ser Ala Gly Pro Arg Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu
 180 185 190
 Cys Met Ser Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile
 195 200 205
 Pro Gln Ala Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu
 210 215 220
 Lys Cys Lys Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu
 225 230 235 240
 Val Pro Arg Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val
 245 250 255
 Cys Gly Thr Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu
 260 265 270

<210> 192
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 192
 Met Pro Pro Ser Ala Phe Leu Phe Phe Phe Trp Arg Gln Ser Leu Ala
 1 5 10 15
 Leu Leu Pro Arg Leu Glu Cys Ser Ser Thr Ile Ser Ala Leu Thr Ala
 20 25 30
 Thr Ser Val Ser Trp Val Gln Ala Ile Leu Leu Pro Gln Pro Pro Lys
 35 40 45
 Tyr Leu Gly Leu Gln Ala Cys Ala Thr Thr Pro Gly
 50 55 60

<210> 193
 <211> 357
 <212> PRT
 <213> Homo sapiens

<400> 193
 Met Pro Ile Leu Thr Gly Asp Phe Leu Leu Pro Thr Pro Gln Phe Tyr
 1 5 10 15
 Ala Glu Asn Ile Asn Thr Thr Ser Leu Thr Cys Ser Ser Asp Arg Met
 20 25 30
 Arg Val Ile Ile Ser Lys Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly
 35 40 45
 Asn Asn Leu Gln Leu Lys Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn
 50 55 60

Val Val Glu Phe Ser Val Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys
 65 70 75 80
 Val Glu Asp Gln Ser Ile Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala
 85 90 95
 Ser Ser Thr Ser Glu Val Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile
 100 105 110
 Val Lys Cys Glu Met Gly His Asn Ser Thr Val Glu Ile Ile Tyr Ile
 115 120 125
 Thr Glu Asp Asp Val Ile Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn
 130 135 140
 Thr Ser Met Ala Leu Phe Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu
 145 150 155 160
 Glu Ser Pro Tyr Tyr Val Asp Leu Asn Gln Thr Leu Phe Val Gln Val
 165 170 175
 Ser Leu His Thr Ser Asp Pro Asn Leu Val Val Phe Leu Asp Thr Cys
 180 185 190
 Arg Ala Ser Pro Thr Ser Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile
 195 200 205
 Lys Ser Gly Cys Ser Arg Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe
 210 215 220
 Gly His Tyr Gly Arg Phe Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser
 225 230 235 240
 Met Ser Ser Val Tyr Leu Gln Cys Lys Val Leu Ile Cys Asp Ser Ser
 245 250 255
 Asp His Gln Ser Arg Cys Asn Gln Gly Cys Val Ser Arg Ser Lys Arg
 260 265 270
 Asp Ile Ser Ser Tyr Lys Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile
 275 280 285
 Arg Leu Lys Arg Asp Arg Ser Ala Ser Gly Asn Ser Gly Phe Gln His
 290 295 300
 Glu Thr His Ala Glu Glu Thr Pro Asn Gln Pro Phe Asn Ser Val His
 305 310 315 320
 Leu Phe Ser Phe Met Val Leu Ala Leu Asn Val Val Thr Val Ala Thr
 325 330 335
 Ile Thr Val Arg His Phe Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln
 340 345 350
 Lys Leu Gln Asn Tyr
 355

<210> 194

<211> 169

<212> PRT

<213> Homo sapiens

<400> 194

Met Gln Cys Leu Leu Pro Tyr Gln Ser Lys Glu Pro Ser Cys Leu Pro
 1 5 10 15

Pro Leu Pro Leu Asn Leu Pro Leu Pro Pro Cys Leu Cys Pro Leu Leu
 20 25 30

Gln Leu Asn Ala Ala Met Thr Arg Lys Glu Lys Thr Lys Glu Gly Gln
 35 40 45

Arg Ala Ala Gln Phe Ser Ala Gly Ala Asp Ala Gly Ser Gly Gly Gly
 50 55 60

Leu Ser Arg Gln Lys Asp Thr Lys Arg Pro Met Leu Leu Val Ile His
 65 70 75 80

Asp Val Val Leu Glu Leu Leu Thr Ser Ser Asp Cys His Ala Asn Pro
 85 90 95

Arg Lys Tyr Pro Thr Cys Gln Lys Ser Glu Val Leu Gly Val Ser Ile
 100 105 110

Tyr Val Ser Ile Cys Pro Ser Thr Arg Pro Arg Asp Lys Asn Lys Thr
 115 120 125

Lys Lys Arg Cys Gln Val Leu Glu Ala Val Leu Val Ser Lys Pro Ser
 130 135 140

Gly Ser Cys His Gln Gly Ser Phe Glu Ile Val Pro His Val Lys Gly
 145 150 155 160

Asn Leu Ala Phe Thr Ser Ser Asn Asn
 165

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/07285

| A. CLASSIFICATION OF SUBJECT MATTER IPC(7) : C12Q 1/68; C12N 15/00, 15/09, 15/63, 15/86 US CL : 435/6, 69.1, 69.3, 320.1, 455, 471; 530/300, 350; 424/189.1 According to International Patent Classification (IPC) or to both national classification and IPC | | |
|---|--|--|
| B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/6, 69.1, 69.3, 320.1, 455, 471; 530/300, 350; 424/189.1 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) EAST, USPATFULL | | |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT | | |
| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| X -- Y | Database EST on STN. Hudson et al. AN X11582. 'New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease' WO 98/20165 see, bases 1-67, which would hybridize to SEQ ID NO: 1. | 1 -- 2-11 |
| X -- Y | Database EST on STN. Hillier et al. AN W51776. 'The WashU-Merck EST Project' 11 October 1996. See Sequence Alignment (attached) disclosing 85% similarity to SEQ ID NO: 1, and would hybridize to SEQ ID NO: 1 | 1 -- 2-11 |
| X -- Y | Database EST on STN. 'NCI-CGAP' AN AA568724. '09 September 1997. See Sequence Alignment (attached) which discloses a polynucleotide with 88% similarity to SEQ ID NO: 1 and would hybridize to SEQ ID NO: 1. | 1 -- 2-11 |
| <input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex. | | |
| * Special categories of cited documents: *A* document defining the general state of the art which is not considered to be of particular relevance *E* earlier document published on or after the international filing date *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *G* document referring to an oral disclosure, use, exhibition or other means *P* document published prior to the international filing date but later than the priority date claimed | *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *A* document member of the same patent family | |
| Date of the actual completion of the international search 27 JUNE 2000 | | Date of mailing of the international search report 19 JUL 2000 |
| Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230 | | Authorized officer MARY K ZEMAN Telephone No. (703) 308-0196 |

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/07285

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---------------------|---|-----------------------|
| X, P --- Y, P | Database Gen EMBL. AN AC009651. Birren et al. 'Homo sapiens chromosome 11, clone' 29 September 1999. See Sequence Alignment (attached) which discloses a polynucleotide having up to 98% identity to SEQ ID NO: 1, and could encode SEQ ID NO: 2. | 1 -- 2-11 |

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/07285**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-11, SEQ ID NO: 1 and 2

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
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BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

- Group I, claim(s) 1-11, drawn to polynucleotides (SEQ ID NO: 1) and encoded polypeptides (SEQ ID NO: 2), and methods of making the recombinant polypeptides.
- Group II, claim(s) 12-13, drawn to polynucleotides (SEQ ID NO: 3) and encoded polypeptides (SEQ ID NO: 4).
- Group III, claim(s) 14-15, drawn to polynucleotides (SEQ ID NO: 5) and encoded polypeptides (SEQ ID NO: 6).
- Group IV, claim(s) 16-17, drawn to polynucleotides (SEQ ID NO: 7) and encoded polypeptides (SEQ ID NO: 8).
- Group V, claim(s) 18-19, drawn to polynucleotides (SEQ ID NO: 9) and encoded polypeptides (SEQ ID NO: 10).
- Group VI, claim(s) 20-21, drawn to polynucleotides (SEQ ID NO: 11) and encoded polypeptides (SEQ ID NO: 12).
- Group VII, claim(s) 22-23, drawn to polynucleotides (SEQ ID NO: 13) and encoded polypeptides (SEQ ID NO: 14).
- Group VIII, claim(s) 24-25, drawn to polynucleotides (SEQ ID NO: 15) and encoded polypeptides (SEQ ID NO: 16).
- Group IX, claim(s) 26-27, drawn to polynucleotides (SEQ ID NO: 17) and encoded polypeptides (SEQ ID NO: 18).
- Group X, claim(s) 28-29, drawn to polynucleotides (SEQ ID NO: 19) and encoded polypeptides (SEQ ID NO: 20).
- Group XI, claim(s) 30-31, drawn to polynucleotides (SEQ ID NO: 21) and encoded polypeptides (SEQ ID NO: 22).
- Group XII, claim(s) 32-33, drawn to polynucleotides (SEQ ID NO: 23) and encoded polypeptides (SEQ ID NO: 24).
- Group XIII, claim(s) 34-35, drawn to polynucleotides (SEQ ID NO: 25) and encoded polypeptides (SEQ ID NO: 26).
- Group XIV, claim(s) 36-37, drawn to polynucleotides (SEQ ID NO: 27) and encoded polypeptides (SEQ ID NO: 28).
- Group XV, claim(s) 38-39, drawn to polynucleotides (SEQ ID NO: 29) and encoded polypeptides (SEQ ID NO: 30).
- Group XVI, claim(s) 40-41, drawn to polynucleotides (SEQ ID NO: 31) and encoded polypeptides (SEQ ID NO: 32).
- Group XVII, claim(s) 42-43, drawn to polynucleotides (SEQ ID NO: 33) and encoded polypeptides (SEQ ID NO: 34).
- Group XVIII, claim(s) 44-45, drawn to polynucleotides (SEQ ID NO: 35) and encoded polypeptides (SEQ ID NO: 36).
- Group XIX, claim(s) 46-47, drawn to polynucleotides (SEQ ID NO: 37) and encoded polypeptides (SEQ ID NO: 38).
- Group XX, claim(s) 48-49, drawn to polynucleotides (SEQ ID NO: 39) and encoded polypeptides (SEQ ID NO: 40).
- Group XXI, claim(s) 50-51, drawn to polynucleotides (SEQ ID NO: 41) and encoded polypeptides (SEQ ID NO: 42).
- Group XXII, claim(s) 52-53, drawn to polynucleotides (SEQ ID NO: 43) and encoded polypeptides (SEQ ID NO: 44).
- Group XXIII, claim(s) 54-55, drawn to polynucleotides (SEQ ID NO: 45) and encoded polypeptides (SEQ ID NO: 46).
- Group XXIV, claim(s) 56-57, drawn to polynucleotides (SEQ ID NO: 47) and encoded polypeptides (SEQ ID NO: 48).
- Group XXV, claim(s) 58-59, drawn to polynucleotides (SEQ ID NO: 49) and encoded polypeptides (SEQ ID NO: 50).
- Group XXVI, claim(s) 60-61, drawn to polynucleotides (SEQ ID NO: 51) and encoded polypeptides (SEQ ID NO: 52).
- Group XXVII, claim(s) 62-63, drawn to polynucleotides (SEQ ID NO: 53) and encoded polypeptides (SEQ ID NO: 54).
- Group XXVIII, claim(s) 64-65, drawn to polynucleotides (SEQ ID NO: 55) and encoded polypeptides (SEQ ID NO: 56).
- Group XXIX, claim(s) 66-67, drawn to polynucleotides (SEQ ID NO: 57) and encoded polypeptides (SEQ ID NO: 58).
- Group XXX, claim(s) 68-69, drawn to polynucleotides (SEQ ID NO: 59) and encoded polypeptides (SEQ ID NO: 60).
- Group XXXI, claim(s) 70-71, drawn to polynucleotides (SEQ ID NO: 61) and encoded polypeptides (SEQ ID NO: 62).
- Group XXXII, claim(s) 72-73, drawn to polynucleotides (SEQ ID NO: 63) and encoded polypeptides (SEQ ID NO: 64).
- Group XXXIII, claim(s) 74-75, drawn to polynucleotides (SEQ ID NO: 65) and encoded polypeptides (SEQ ID NO: 66).
- Group XXXIV, claim(s) 76-77, drawn to polynucleotides (SEQ ID NO: 67) and encoded polypeptides (SEQ ID NO: 68).
- Group XXXV, claim(s) 78-79, drawn to polynucleotides (SEQ ID NO: 69) and encoded polypeptides (SEQ ID NO: 70).
- Group XXXVI, claim(s) 80-81, drawn to polynucleotides (SEQ ID NO: 71) and encoded polypeptides (SEQ ID NO: 72).
- Group XXXVII, claim(s) 82-83, drawn to polynucleotides (SEQ ID NO: 73) and encoded polypeptides (SEQ ID NO: 74).
- Group XXXVIII, claim(s) 84-85, drawn to polynucleotides (SEQ ID NO: 75) and encoded polypeptides (SEQ ID NO: 76).
- Group XXXIX, claim(s) 86-87, drawn to polynucleotides (SEQ ID NO: 77) and encoded polypeptides (SEQ ID NO: 78).
- Group XXXX, claim(s) 88-89, drawn to polynucleotides (SEQ ID NO: 79) and encoded polypeptides (SEQ ID NO: 80).
- Group XXXXI, claim(s) 90-91, drawn to polynucleotides (SEQ ID NO: 81) and encoded polypeptides (SEQ ID NO: 82).
- Group XXXXII, claim(s) 92-93, drawn to polynucleotides (SEQ ID NO: 83) and encoded polypeptides (SEQ ID NO: 84).
- Group XXXXIII, claim(s) 94-95, drawn to polynucleotides (SEQ ID NO: 85) and encoded polypeptides (SEQ ID NO: 86).

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- 86).
Group XXXXIV, claim(s) 96-97, drawn to polynucleotides (SEQ ID NO: 87) and encoded polypeptides (SEQ ID NO: 88).
Group XXXXV, claim(s) 98-99, drawn to polynucleotides (SEQ ID NO: 89) and encoded polypeptides (SEQ ID NO: 90).
Group XXXXVI, claim(s) 100-101, drawn to polynucleotides (SEQ ID NO: 91) and encoded polypeptides (SEQ ID NO: 92).
Group XXXXVII, claim(s) 102-103, drawn to polynucleotides (SEQ ID NO: 93) and encoded polypeptides (SEQ ID NO: 94).
Group XXXXVIII, claim(s) 104-105, drawn to polynucleotides (SEQ ID NO: 95) and encoded polypeptides (SEQ ID NO: 96).
Group XXXXIX, claim(s) 106-107, drawn to polynucleotides (SEQ ID NO: 97) and encoded polypeptides (SEQ ID NO: 98).
Group L, claim(s) 108-109, drawn to polynucleotides (SEQ ID NO: 99) and encoded polypeptides (SEQ ID NO: 100).
Group LI, claim(s) 101-111, drawn to polynucleotides (SEQ ID NO: 101) and encoded polypeptides (SEQ ID NO: 102).
Group LII, claim(s) 112-113, drawn to polynucleotides (SEQ ID NO: 103) and encoded polypeptides (SEQ ID NO: 104).
Group LIII, claim(s) 114-115, drawn to polynucleotides (SEQ ID NO: 105) and encoded polypeptides (SEQ ID NO: 106).
Group LIV, claim(s) 116-117, drawn to polynucleotides (SEQ ID NO: 107) and encoded polypeptides (SEQ ID NO: 108).
Group LV, claim(s) 118-119, drawn to polynucleotides (SEQ ID NO: 109) and encoded polypeptides (SEQ ID NO: 110).
Group LVI, claim(s) 120-121, drawn to polynucleotides (SEQ ID NO: 111) and encoded polypeptides (SEQ ID NO: 112).
Group LVII, claim(s) 122-123, drawn to polynucleotides (SEQ ID NO: 113) and encoded polypeptides (SEQ ID NO: 114).
Group LVIII, claim(s) 124-125, drawn to polynucleotides (SEQ ID NO: 115) and encoded polypeptides (SEQ ID NO: 116).
Group LIX, claim(s) 126-127, drawn to polynucleotides (SEQ ID NO: 117) and encoded polypeptides (SEQ ID NO: 118).

The inventions listed as Groups ONE (I) to FIFTY NINE (LIX) do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each polynucleotide and corresponding polypeptide do not share any sequence homology, similar structure or other feature which could be considered a special technical feature. Each polynucleotide sequence and corresponding polypeptide sequence is a separate and distinct invention, having no obvious shared features, and thus, lack unity under PCT Rule 13.2.